

## **Descriptions of Barley Genetic Stocks for 2012**

**Jerome D. Franckowiak<sup>1</sup> and Udda Lundqvist<sup>2</sup>**

**<sup>1</sup>Department of Agriculture, Fisheries and Forestry  
Hermitage Research Facility, Agri-Science Queensland  
Warwick, Queensland 4370, Australia**

**<sup>2</sup>Nordic Genetic Resource Center (Nordgen)  
P.O. Box 41, SE-230 53 Alnarp, Sweden**

This volume of the Barley Genetics Newsletter (BGN) includes an updated compilation of the Barley Genetic Stock (BGS) descriptions. At the workshops of the 11th International Barley Genetics Symposium held 15-20 April 2012 at Hangzhou, China, it was recommended that existing BGS descriptions be published in one volume. This action was taken because many descriptions lacked updated information on where seed stocks are held and some difficulties existed in rapidly locating the latest revision for each description. Revised symbolizations for barley chromosomes, loci and alleles were approved at the 7th International Barley Genetics Symposium held 30 July to August 6 1996 at Saskatoon, Saskatchewan. The changes were applied in the compilation of BGS descriptions published in Volume 26 in the BGN (Davis et al. 1997). Since then more new and revised BGS descriptions have been published in different volumes of BGN. The BGS descriptions included in Volume 42 of the BGN were modified to identify current sources of seed stocks with its GSHO number and/or NGB number. The GSHO stocks are held in the USDA-ARS Barley Genetic Stocks collection at the National Small Grains Collection, U.S. Department of Agriculture – Agricultural Research Service, National Small Grains Germplasm Research Facility, 1691 S 2700 W, Aberdeen, ID 83210, USA. The NGB and Bowman backcross-derived (BW) stocks are held in the Nordic Genetic Resource Center (Nordgen), P.O. Box 41, SE-230 53 Alnarp, Sweden.

A brief outline of historic efforts to describe and map barley genes provides a background for the changes made in BGS descriptions presented in this volume of BGN. When the first volume of the BGN was published in 1971, the editors (Tom Ramage, Ted Haus, and Tak Tsuchiya) included descriptions of simply inherited morphological traits present in stocks held at Colorado State University (Tsuchiya et al., 1971). For morphological variants at each locus, the BGS descriptions summarized inheritance patterns, linkage data, morphological effects, origins, seed sources, and literature references. The BGS descriptions expanded in a different format the previous reviews of barley genetics published by Nilan, 1964; Robertson et al., 1941, 1965; and Smith, 1951. In these reviews the history of barley genetics can be traced back to the genetic studies on the black lemma and pericarp 1 (*Blp1*) locus, which were published soon after the rediscovery of Mendel's principles of inheritance (Tschermak, 1901). To make working with the BGS descriptions easier, many of the BGS descriptions were corrected and updated in Volume 26 of BGN (Davis et al. 1997).

The current lists of new and revised BGS descriptions are presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in another section of this issue. Information on the description location, recommended locus name, chromosomal location,

previous gene symbols, and the primary genetic stock (GSHO number) are included in these tables. All this information is available through the Internet at the following addresses:

- (1) [www.ars.usda.gov.PacWest/Aberdeen](http://www.ars.usda.gov.PacWest/Aberdeen)
- (2) [www.ars-grin.gov:7000/npgs/descriptors/barley-genetics](http://www.ars-grin.gov:7000/npgs/descriptors/barley-genetics) (GRIN)
- (3) <http://wheat.pw.usda.gov/ggpages/bgn/>
- (4) <http://www.nordgen.org/sesto>
- (5) <http://ace.untamo.net>

#### References:

- Davis, M.P., J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997.** Barley Genetics Newsletter, Volume 26. American Malting Barley Association, Inc., Milwaukee, WI.
- Nilan, R.A. 1964.** The Cytology and Genetics of Barley, 1951-1962. Monographic Supplement No. 3 Research Studies. Washington State University Press.
- Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941.** A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.
- Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965.** A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III, 1954-1963. Crop Sci. 5:33-43.
- Smith, L. 1951.** Cytology and genetics of barley. Bot. Rev. 17:1-51, 133-202, 285-355.
- Tschermak, E. von. 1901.** Über Züchtung neuer Getreiderassen mittelst künstlicher Kreuzung. Kritisch-historische Betrachtungen. Zeitschrift für das landwirtschaftliche Versuchswesen Oesterreich 4:1029-1060.
- Tsuchiya, T., T.E. Haus, et al. 1971.** Description of genetic stocks in the Barley Genetic Stock Center at Fort Collins, Colorado. Barley Genet. Newsl. 1:103-193.

# BGS 1, Brachytic 1, *brh1*

Stock number: BGS 1  
Locus name: Brachytic 1  
Locus symbol: *brh1*

## Previous nomenclature and gene symbolization:

Brachytic = *br* (11, 13).  
Breviaristatum-*i* = *ari-i* (6, 9).  
Dwarf x = *dx1* (7).

## Inheritance:

Monofactorial recessive (11, 13).  
Located in chromosome 7HS (4); about 9.3 cM distal from the *fch12* (chlorina seedling 12) locus (13); 0.8 cM distal from RFLP marker BCD129 (10); about 5.0 cM from AFLP marker E4134-8 in subgroup 1 of the Proctor/Nudinka map (12); about 13.6 cM proximal from SSR marker HVM04 in 7H bin 02 (2); *brh1.a* is associated with SNP markers 2\_1419 to 2\_0245 (positions 0.00 to 13.19 cM) in 7H bin 01 of the Bowman backcross-derived line BW074 (3); *brh1.x* is associated with SNP markers 1\_0949 to 1\_1495 (positions 0.00 to 8.77 cM) in 7H bin 01 of the Bowman backcross-derived line BW079 (3); *brh1.t* is associated with SNP markers 1\_1495 to 1\_0025 (positions 8.77 to 26.00 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW078 (3); an unnamed *brh1* mutant is associated with SNP markers 1\_0851 to 2\_0485 (positions 17.32 to 121.90 cM) in 7H bins 02 to 07 of the Bowman backcross-derived line BW872 (3), likely in 1H bin 01 near the border with 1H bin 02.

## Description:

Plants have short leaves, culms, spikes, awns, and kernels. The seedling leaf is about 2/3 normal length. A similar reduction in the size of other organs is observed, but the awns were less than 1/2 normal length (7). The mutant phenotype was easy to classify at all stages of growth. The approximately 20% reduction in kernel weight was caused primarily by a reduction in kernel length, 7.8 vs. 9.6 mm. Grain yields of the Bowman backcross-derived lines for *brh1* mutants were about 2/3 normal and lodging was greatly reduced (2). Börner (1) reported that *ari-i.38* seedlings are sensitive to gibberellic acid. Powers (11) stated that the assigned gene symbol for this mutant is *br* and that L.J. Stadler selected this symbol.

## Origin of mutant:

A spontaneous mutant in Himalaya (Clho 1312) (11, 13).

## Mutational events:

*brh1.a* (GSHO 25) in Himalaya (13); *brh1.c* (GSHO 229) in Moravian (PI 539135) (14); *ari-i.38* (NGB 115888, GSHO 1657) in Bonus (PI 189763) (9, 15); *brh1.e* (GSHO 1690) in Aramir (PI 467786) (15); *brh1.f* (*dx1*, GSHO 1422) in Domen (Clho 9562) (7); *brh1.t* (OUM136, GSHO 1691) in Akashinriki (PI 467400, OUJ659); *brh1.x* (7125, GSHO 1692) in Volla (PI 280423); *brh1.z* (Hja80001) in Aapo; *brh1.aa* (Hja80051) in a Hja80001 cross (5, 8); *brh1.ae* (FN053) in Steptoe (Clho 15229) (5); an unnamed variant in L50-200 (Alb Acc 67A, GSHO 1217) (16).

## Mutant used for description and seed stocks:

*brh1.a* in Himalaya (GSHO 25); *ari-i.38* (GSHO 1657, NGB 115888) in Bonus, *brh1.a* in Bowman (PI 483237)\*7 (GSHO 1820, BW074, NGB 20481); *ari-i.38* in Bowman\*6 (GSHO 1821, BW047, NGB 20455); *brh1.e* in Bowman\*7 (GSHO 1822, BW077, NGB 20484); *brh1.t* in Bowman\*7 (GSHO 1823, BW078, NGB 20485); *brh1.x* in Bowman\*7 (GSHO 1824, BW079, NGB 20486); *brh1.z* in Bowman\*7 (GSHO 2179, BW080, NGB

20487); *brh1.aa* in Bowman\*6 (GSHO 1668, BW075, NGB 20482); *brh1.ae* in Bowman\*4 (BW076, NGB 20483).

References:

1. Börner, A. 1996. GA response in semidwarf barley. *Barley Genet. Newsl.* 25:24-26.
2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
4. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. *Can. J. Genet. Cytol.* 14:949-957.
5. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
6. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
7. Holm, E., and K. Aastveit. 1966. Induction and effects of the brachytic allele in barley. *Adv. Front Plant Sci.* 17:81-94.
8. Kivi, E. 1986. (Personal communications).
9. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of brevistaratum mutants in barley. *Hereditas* 80:263-278.
10. Li, M., D. Kudrna, and A. Kleinhofs. 2000. Fine mapping of a semi-dwarf gene brachytic 1 in barley. p. 72-74. *In* S. Logue (ed.) *Barley Genetics VIII. Volume III, Proc. Eighth Int. Barley Genet. Symp.*, Adelaide, Dept. Plant Science, Waite Campus, Adelaide University, Glen Osmond, South Australia.
11. Powers, L. 1936. The nature of the interactions of genes affecting four quantitative characters in a cross between *Hordeum deficiens* and *vulgare*. *Genetics* 21:398-420.
12. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.
13. Swenson, S.P. 1940. Genetic and cytological studies on a brachytic mutant in barley. *J. Agric. Res.* 60:687-713.
14. Szarejko, I., and M. Maluszynski. 1984. New brachytic mutant of spring barley variety Aramir. *Barley Genet. Newsl.* 14:33-35.
15. Tsuchiya, T. 1974. Allelic relationships of genes for short-awned mutants in barley. *Barley Genet. Newsl.* 4:80-81.
16. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. *Can. J. Genet. Cytol.* 5:200-219.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:104.

Revised:

- T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:100.  
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:44.  
J.D. Franckowiak and L. S. Dahleen. 2007. *Barley Genet. Newsl.* 37:188-189.  
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:58-59.

BGS 2, Chlorina seedling 12, *fch12*

Stock number: BGS 2  
Locus name: Chlorina seedling 12  
Locus symbol: *fch12*

Previous nomenclature and gene symbolization:

Chlorina seedling-c = *f<sub>c</sub>* (5).  
Chlorina seedling-fc = *clo-fc* (9).

Inheritance:

Monofactorial recessive (5).  
Located in chromosome 7HS (2, 6); about 3.6 cM distal from the *gsh3* (glossy sheath 3) locus (8); about 9.3 cM proximal from the *brh1* (brachytic 1) locus (10); in 7H bin 02 about 2.3 cM from RFLP marker KFP027 and co-segregating with markers BCD130 and ABC327 (7); *fch12.b* is associated with SNP markers 2\_0242 to 2\_0495 (positions 6.89 to 32.35 cM) in 7H bins 01 to 03 of the Bowman backcross-derived line BW354 (1), in 7H bin 02.

Description:

Seedling leaves are yellow with green tips and new leaves show a yellow base and a green tip. As the plant develops, leaf color changes to pale green (5). Plants are vigorous, but anthesis is delayed by 6 to 10 days. Kernel weights of BW354 vary from similar to those of Bowman to 10% less. Grain production of BW354 is 1/2 to 2/3 of that of Bowman (3).

Origin of mutant:

A spontaneous mutant in Colseess (Clho 2792) (5).

Mutational events:

*fch12.b* (*f<sub>c</sub>*) in Colseess (Colseess V, GSHO 36) (5); *fch12.l* (Trebi chlorina 453, GSHO 155), *fch12.m* (Trebi V, GSHO 158), *fch12.n* (Trebi IX, GSHO 18), *fch12.o* (Trebi XI, GSHO 163) in Trebi (PI 537442) (4); *clo-fc.110* in Bonus (PI 189763) (9); *fch12.b* may be present in the brachytic chlorina stocks (GSHO 124 and GSHO 174) (11).

Mutant used for description and seed stocks:

*fch12.b* in Colseess (GSHO 36); *fch12.b* in Bowman (PI 483237)\*7 (GSHO 1826); *fch12.b* in Bowman\*8 (BW354, NGB 20593).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. *Can. J. Genet. Cytol.* 14:949-957.
3. Franckowiak, J.D. (Unpublished).
4. McMullen, M. 1972. Allelism testing of seven chlorina mutants in Trebi barley. *Barley Genet. Newsl.* 2:76-79.
5. Robertson, D.W., and G.W. Deming. 1930. Genetic studies in barley. *J. Hered.* 21:283-288.
6. Robertson, D.W., G.W. Deming, and D. Koonce. 1932. Inheritance in barley. *J. Agric. Res.* 44:445-466.
7. Schmierer, D., A. Druka, D. Kudrna, and A. Kleinhofs. 2001. Fine mapping of the *fch12* chlorina seedling mutant. *Barley Genet. Newsl.* 31:12-13.
8. Shahla, A., and T. Tsuchiya. 1987. Cytogenetic studies in barley chromosome 1 by means of telotrisomic, acrotriosomic and conventional analysis. *Theor. Appl. Genet.* 75:5-12.

9. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). Carlsberg Res. Commun. 50:223-238.
10. Swenson, S.P. 1940. Genetic and cytological studies on a brachytic mutation in barley. J. Hered. 31:213-214.
11. Wang, S., and T. Tsuchiya. 1991. Genetic analysis of the relationship between new chlorina mutants in genetic stocks and established *f* series stocks in barley. Barley Genet. Newsl. 20:63-65.

Prepared:

T. Tsuchiya and T. E. Haus. 1971. Barley Genet. Newsl. 1:105.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:101.

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:45.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:190-191.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:60-61.

BGS 3, Virescent seedling 2, *yvs2*

Stock number: BGS 3  
Locus name: Virescent seedling 2  
Locus symbol: *yvs2*

Previous nomenclature and gene symbolization:

Virescent seedling-c =  $y_c$  (2).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 7HS (2); about 24.4 cM proximal from the *gsh3* (glossy sheath 3) locus (3); 17.0 cM distal from the *cer-f* (eceriferum-f) locus (3).

Description:

The seedling leaf is white with a very marked green tip, which remains green. The green area on the second leaf is very small or lacking. Homozygous recessive seedlings seldom survive beyond the two leaf stage (1). The *yvs2.c* gene is generally maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Coast (PI 539103) (1).

Mutational events:

*yvs2.c* (GSHO 41, Coast III) in Coast (PI 539103) (1).

Mutant used for description and seed stocks:

*yvs2.c* (GSHO 41) in Coast.

References:

1. Robertson, D.W., and G.W. Deming. 1930. Genetic studies in barley. J. Hered. 21:283-288.
2. Robertson, D.W., G.W. Deming, and D. Koonce. 1932. Inheritance in barley. J. Agric. Res. 44:445-466.
3. Sogaard, B. 1973. Continued linkage studies on *eceriferum* mutants in barley. Barley Genet. Newsl. 3:57-61.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:106.

Revised:

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:46.

BGS 4, Albino seedling 8, *abo8*

Stock number: BGS 4  
Locus name: Albino seedling 8  
Locus symbol: *abo8*

Previous nomenclature and gene symbolization:

White seedling c2 = *a<sub>c2</sub>* (4).  
Albino seedling c2 = *a<sub>c2</sub>* (5).  
Albina seedling-m = *alb-m* (7).

Inheritance:

Monofactorial recessive (2, 4).  
Located in chromosome 7HS (1, 3, 6); about 27.2 cM distal from the *nud1* (naked caryopsis 1) locus (2); over 11.3 cM distal from the *nud1* locus (1); about 18.0 cM distal from the *fch8* (chlorina seedling 8) locus (3).

Description:

Seedlings are white in color and devoid of normal pigments (4). Plants with this phenotype are classified as albino mutants (5). The *abo8.h* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Coast (PI 539103) (2, 4).

Mutational events:

*abo8.h* (GSHO 61, Coast II) in Coast (PI 539103) (4); *alb-m.27* (NGB 14701) in Bonus (PI 539132) (7, 8).

Mutant used for description and seed stocks:

*abo8.h* (GSHO 61) in Coast.

References:

1. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. *Hereditas* 62:25-96.
2. Robertson, D.W. 1937. Maternal inheritance in barley. *Genetics* 22:104-113.
3. Robertson, D.W. 1967. Linkage studies of various barley mutations (*Hordeum* species). *Crop Sci.* 7:41-42.
4. Robertson, D.W., and G.W. Deming. 1930. Genetic studies in barley. *J. Hered.* 21:283-288.
5. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. *J. Am. Soc. Agron.* 33:47-64.
6. Shahla, A., and T. Tsuchiya. 1982. Telotrisomic analysis of the gene *a<sub>c2</sub>* (albino seedling) in Triplo 1L in barley. *Barley Genet. Newsl.* 12:32-33.
7. Wettstein, D. von, and K. Kristiansen. 1973. Stock list for nuclear gene mutants affecting the chloroplast. *Barley Genet. Newsl.* 3:113-117.
8. Wettstein, D. von, and K. Kristiansen. 1975. Report by coordinators on chloroplast genes: Progress report II on diallelic tests between mapped chloroplast genes and chloroplast genes in stock collection at Copenhagen. *Barley Genet. Newsl.* 5:90-91.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:107.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:47.



BGS 5, Chlorina seedling 8, *fch8*

Stock number: BGS 5  
Locus name: Chlorina seedling 8  
Locus symbol: *fch8*

Previous nomenclature and gene symbolization:

Chlorina seedling 8 = *f8* (4).  
Chlorina seedling-f8 = *clo-f8<sup>f8</sup>* (6).

Inheritance:

Monofactorial recessive (4).  
Located in chromosome 7HS (2, 4, 5); about 13.0 cM distal from the *nud1* (naked caryopsis 1) locus (2, 4); about 2.7 cM distal from the *msg10* (male sterile genetic 10) locus (2); *fch8.j* is associated with SNP markers 1\_1014 to 2\_0445 (positions 80.65 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcrossed-derived line BW105 (1), likely in 7H bin 06.

Description:

Seedlings have a yellow-green color and plants retain a chlorina (yellow green) phenotype until ripening (2). Plants of Bowman backcross-derived line BW105 were viable in the field, but heading was delayed 2 to 10 days across environments. Plant height of BW105 varied from slight taller than Bowman to 3/3 of Bowman height and awns were slightly shorter. Spikes of BW105 had 2 to 3 more kernels than those of Bowman, seed weights were approximately 10% lower. Grain yields were 1/2 to 3/4 of those of Bowman (3).

Origin of mutant:

A spontaneous mutant in Comfort (Clho 4578) (4).

Mutational events:

*fch8.j* (GSHO 40, Comfort No II) in Comfort (Clho 4578) (4).

Mutant used for description and seed stock:

*fch8.j* (GSHO 40) in Comfort; *fch8.j* in Bowman (PI 483237)\*8 (GSHO 1829, BW364, NGB 20603).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Eslick, R.F. 1976. Approximate position of the chlorina mutants *f4f4* and *f8f8* on chromosome 1. *Barley Genet. Newsl.* 6:10-13
3. Franckowiak, J.D. (Unpublished).
4. Robertson, D.W. 1969. Linkage studies with five naturally occurring chlorophyll mutations in barley (*Hordeum* species). *Can. J. Genet. Cytol.* 9:321-326.
5. Shahla, A., and T. Tsuchiya. 1987. Cytogenetic studies in barley chromosome 1 by means of telotrisomic, acrotrisomic and conventional analysis. *Theor. Appl. Genet.* 75:5-12.
6. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). *Carlsberg Res. Commun.* 50:223-238.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:108.

Revised:

T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:102.  
J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:48.  
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:62.

BGS 6, Six-rowed spike 1, *vrs1*

Stock number: BGS 6  
 Locus name: Six-rowed spike 1  
 Locus symbol: *vrs1*

Previous nomenclature and gene symbolization:

Two-row vs six-row = *Zz* (21).  
 Six-row vs two-row = *Aa* (6).  
 Two-rowed = *D* (17).  
 Six-row vs two-row = *Vv* (3).  
 Six-row vs two-row (*distichon*) vs two-row (*deficiens*) = *A*, *a<sup>s</sup>*, *a<sup>f</sup>* (8).  
 Reduced lateral spikelet appendage on the lemma = *lr* (9).  
 Allelic series *v*, *V<sup>d</sup>*, *V*, and *V<sup>t</sup>* (22).  
 Hexastichon mutants = *hex-v* (5, 6).  
 Intermedium spike-d = *Int-d* (4).  
 Reduced lateral spikelet appendage on the lemma = *v<sup>r</sup>* (19).  
 The *vrs1* DNA sequence identified as *HvHox1* (10).

Inheritance:

A multiple allelic series, incomplete dominant allele interactions based on the size and shape of lateral spikelets (1, 19, 22).  
 Located in chromosome 2HL (3, 6, 12, 14); about 30.5 cM distal from the *eog1* (elongated outer glume 1) locus (18), in 2H bin 09 and in a 0.90-cM interval between markers cMWG699 and MWG865 (11).

Description:

Alleles at this complex locus modify development of the lateral spikelets and the associated lemma awn. The *vrs1.a* allele (*v* gene) is present in most six-rowed cultivars and produces well-developed lateral spikelets (6). Based on phylogenetic analysis of the six-rowed cultivars, the six-rowed gene originated independently at least three times (*vrs1.a1*, *vrs1.a2*, and *vrs1.a3*) from different wild type (*Vrs1.b*) alleles (10). The lemma awn of lateral spikelets will vary from 3/4 to nearly as long as those of central spikelets, depending upon alleles present at other loci. The *Vrs1.b* allele (*V* gene, *distichon*) is present in many two-rowed cultivars and reduces lateral spikelets to sterile bracts with a rounded tip. The *Vrs1.t* allele (*V<sup>t</sup>* gene, *deficiens*) causes an extreme reduction in the size of lateral spikelets. The *lr* or *v<sup>r</sup>* (*vrs1.c*) gene in Nudihaxtoni and Bozu types will not recombine with the *vrs1.a* allele (12, 19) and produces phenotypes similar to the *Vrs1.d* allele (*V<sup>d</sup>* gene) of Svanhals (22). The series of induced mutants in two-rowed barley called *hex-v* and *Int-d* mutants differ in the size of lateral spikelets, but they interact with the *vrs1.a* allele as incomplete dominants (5). Many heterozygous combinations with *vrs1.a* have a pointed tip on the lemma of sterile lateral spikelets. Alleles at the *int-c* (intermedium spike-c) locus modify lateral size in the presence of *vrs1.a*, *Vrs1.b*, and *Vrs1.d*, but not when *Vrs1.t* is present (22). Multiple origins of *vrs1* alleles in six-rowed barley have been confirmed by molecular analysis (20). Komatsuda et al. (10) found that expression of the *Vrs1* gene was strictly localized in the lateral-spikelet primordia of immature spikes and suggested that the VRS1 protein suppresses development of lateral spikelets.

Origin of mutant:

Natural occurrence in six-rowed barley and induced frequently by mutagenic agents (10, 14).

Mutational events:

*vrs1.a1* in most six-rowed cultivars (1, 10, 22); *vrs1.a2* in Dissa and Valenci (10), *vrs1.a3*

in Natsudaikon Mugi (OUK735) (10), *Vrs1.b* in wild barley (10), *Vrs1.b2* in Pamella Blue (OUH630) (10), *Vrs1.b3* in Bonus (PI 189763) (10), *Vrs1.t* in a few two-rowed cultivars (10, 22); *vrs1.c* or *lr* in Nudihaxtoni (PI 32368) (12, 19); *Vrs1.d* in Svanhals (PI 5474) (22); 23 induced mutants from programs in Belgium, Germany, and Hungary (2); *hex-v.3* (NGB 115545), -v.4 (NGB 115546), -v.6 (NGB 115547), -v.7 (NGB 115548), -v.8 (NGB 115549), -v.9 (NGB 115550), -v.10 (NGB 115551), -v.11 (NGB 115552), -v.12 (NGB 115553), -v.18 (NGB 115559), -v.44 (NGB 115581), -v.45 (NGB 115582), -v.46 (NGB 115583), -v.47 (NGB 115584), -v.48 (NGB 115585), in Bonus, -v.13 (NGB 115554), -v.14 (NGB 115555), -v.15 (NGB 115556), -v.16 (NGB 115557), -v.17 (NGB 115558), -v.19 (NGB 115560), -v.21 (NGB 115562), -v.22 (NGB 115563), -v.23 (NGB 115564), -v.24 (NGB 115565), -v.25 (NGB 115566), -v.26 (NGB 115567), -v.27 (NGB 115568), -v.28 (NGB 115569), -v.29 (NGB 115570), -v.30 (NGB 115571), -v.31 (NGB 115572), -v.35 (NGB 115574) in Foma (CIho 11333), -v.20 (NGB 115561) in Ingrid (CIho 10083), -v.33 (NGB 115573), -v.36 (NGB 115575), -v.38 (NGB 115576), -v.39 (NGB 115577), -v.41 (NGB 115578), -v.42 (NGB 115579), -v.43 (NGB 115580) in Kristina (NGB 1500) (5, 14); *hex-v.49* (NGB 115586) in Bonus, -v.50 (NGB 115587), -v.51 (NGB 115588) in Sv 79353, -v.52 (NGB 119353) in Golf (PI 488529) (13); *Int-d.11* (NGB 115429), -d.12 (NGB 115430), -d.22 (NGB 115440), -d.24 (NGB 115442), -d.28 (NGB 115446), -d.36 (NGB 115454) in Foma, -d.40 (NGB 115458), -d.41 (NGB 115459), -d.50 (NGB 115468), -d.57 (NGB 115475), -d.67 (NGB 115485), -d.68 (NGB 115486), -d.69 (NGB 115487) in Kristina (5, 15); *Int-d.73* (NGB 115491), -d.80 (NGB 115498), -d.82 (NGB 115500) in Bonus, -d.93 (NGB 115511), -d.94 (NGB 115512), -d.96 (NGB 115514), -d.97 (NGB 115515), -d.100 (NGB 115518) in Hege (NGB 13692) (13); *vrs1.o* (*v1b*) in New Golden (16).

Mutant used for description and seed stock:

*vrs1.a* in Trebi (PI 537442, GSHO 196); *vrs1.a* in Bonneville (CIho 7248) (7); *vrs1.a* from Glenn (CIho 15769) in Bowman (PI 483237)\*8 (GSHO 1907, BW898, NGB 22330); *Int-d.12* in Bowman\*7 (GSHO 1910, BW422, NGB 20655).

References:

1. Biffen, R.H. 1906. Experiments on the hybridization of barleys. Proc. Camb. Phil. Soc. 13:304-308.
2. Fukuyama, T., J. Hayashi, I. Moriya, and R. Takahashi. 1972. A test for allelism of 32 induced six-rowed mutants. Barley Genet. Newsl. 2:25-27.
3. Griffiee, F. 1925. Correlated inheritance of botanical characters in barley, and manner of reaction to *Helminthosporium sativum*. J. Agric. Res. 30:915-935.
4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
5. Gustafsson, Å., and U. Lundqvist. 1980. Hexastichon and intermedium mutants in barley. Hereditas 92:229-236.
6. Harlan, H.V., and H.K. Hayes. 1920. Occurrence of the fixed intermediate, *Hordeum intermedium haxtoni*, in crosses between *H. vulgare pallidum* and *H. distichum palmella*. J. Agric. Res. 19:575-591.
7. Hockett, E.A. 1985. Registration of two- and six-rowed isogenic Bonneville barley germplasm. Crop Sci. 25:201.
8. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
9. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.
10. Komatsuda, T., M. Pourkheirandish, C. He, P. Azhaguvel, H. Kanamori, D. Perovic, N. Stein, A. Graner, T. Wicker, A. Tagiri, U. Lundqvist, T. Fujimura, M. Matsuoka, T. Matsumoto, and M. Yano. 2007. Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. PNAS 104:1424-1429.

11. Komatsuda, T., and K. Tanno. 2004. Comparative high resolution map of the six-rowed locus 1 (*vrs1*) in several populations of barley, *Hordeum vulgare* L. *Hereditas* 141:68-73.
12. Leonard, W.H. 1942. Inheritance of reduced lateral spikelet appendages in the Nudihaxtoni variety of barley. *J. Am. Soc. Agron.* 34:211-221.
13. Lundqvist, U. (Unpublished).
14. Lundqvist, U., and A. Lundqvist. 1987. Barley mutants - diversity and genetics. p. 251-257. *In* S. Yasuda and T. Konishi (eds.) *Barley Genetics V. Proc. Fifth Int. Barley Genet. Symp.*, Okayama, 1986. Sanyo Press Co., Okayama.
15. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.
16. Makino, T., M. Furusho, and T. Fukuoka. 1995. A mutant having six-rowed gene allelic to *v* locus. *Barley Genet. Newsl.* 24:122.
17. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] *Bot. Mag., Tokyo* 36:25-38. [In Japanese.]
18. Swenson, S.P., and D.G. Wells. 1944. The linkage relation of four genes in chromosome 1 of barley. *J. Am. Soc. Agron.* 36:429-435.
19. Takahashi, R., J. Hayashi, I. Moriya, and S. Yasuda. 1982. Studies on classification and inheritance of barley varieties having awnless or short-awned lateral spikelets (Bozu barley). I. Variation of awn types and classification. *Nogaku Kenyu* 60:13-24. [In Japanese with English summary.]
20. Tanno, K., S. Taketa, K. Takeda, and T. Komatsuda. 2002. A DNA marker closely linked to the *vrs1* locus (row-type gene) indicates multiple origins of six-rowed barley (*Hordeum vulgare* L.) *Theor. Appl. Genet.* 104:54-60.
21. Ubisch, G. von. 1916. Beitrag zu einer Faktorenanalyse von Gerste. *Z. Indukt. Abstammungs. Vererbungs.* 17:120-152.
22. Woodward, R.W. 1949. The inheritance of fertility in the lateral florets of the four barley groups. *Agron. J.* 41:317-322.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:106.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:49-50.

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:192-194.

BGS 7, Naked caryopsis 1, *nud1*

Stock number: BGS 7  
Locus name: Naked caryopsis 1  
Locus symbol: *nud1*

Previous nomenclature and gene symbolization:

Naked caryopsis = *k* (14).  
Naked caryopsis = *s* (21).  
Naked caryopsis = *n* (6, 9).  
Hulless = *h* (10).

Inheritance:

Monofactorial recessive (6, 14, 19).  
Located in chromosome 7HL (3, 11, 12, 14, 20); near the centromere (3, 11); about 9.6 cM proximal from the *lks2* (short awn 2) locus (15); about 10.5 cM proximal from the *dsp1* (dense spike 1) locus (15, 16); in bin 7H-07 about 13.1 cM distal from RFLP marker MWG808 (2); co-segregating with AFLP markers KT3 and KT7 and SCAR marker sKT7 (7); about 0.06 cM distal from SCAR marker sTK3 and the same distance proximal from sTK9 (17).

Description:

The lemma and palea do not adhere to the caryopsis and the grain will thresh free of the hull at maturity. The naked caryopsis trait is expressed in all environments (16). The naked lines fail to produce a cementing substance present in covered lines (4). The *nud1.a* mutant depressed the expression by 10 to 20% of other traits such as plant height, seed weight (1, 8) and altered malt quality parameters (8). The *nud1.a* gene is often associated with the *dsp1.a* (dense spike 1) gene in Japanese cultivars (16). Allele *IV* of the marker sKT7 near the *nud1* locus was the only one found in naked barley cultivars (18); however, the geographic distribution for haplotypes of allele *IV* suggest migration of naked types toward eastern Asia (18).

Origin of mutant:

In an unknown cultivar, but its origin was monophyletic probably in southwestern Iran (18), widespread in cultivated barley in Asia.

Mutational events:

*nud1.a* (GSHO 115) in Himalaya (CIho 1312) (21); *nud1.b* (Mut 4129) in Haisa, *nud1.c* (Mut 3041/62) in Ackermann's Donaria (PI 161974) (13).

Mutant used for description and seed stocks:

*nud1.a* (GSHO 115) in Himalaya, *nud1.a* from Sermo (CIho 7776) in Betzes (PI 129430)\*7 (CIho 16559, GP 37), *nud1.a* from Sermo in Compana (CIho 5438)\*7 (CIho 16185, GP 41), *nud1.a* from Sermo in Decap (CIho 3351)\*7 (CIho 16563, GP 45) (5); *nud1.a* from Stamm (PI 194555) in Betzes\*7 (CIho 16566, GP 48), *nud1.a* from Stamm in Compana\*7 (CIho 16183, GP 50), *nud1.a* from Stamm\*7 in Freja (CIho 7130)\*7 (CIho 16568, GP 52) (5); *nud1.a* from a Chinese introduction in Bowman (PI 483237)\*8 (GSHO 1847, BW638, NGB 20751).

References:

1. Choo, T-M., K.M. Ho, and R.A. Martin. 2001. Genetic analysis of a hulless X covered cross of barley using doubled-haploid lines. *Crop Sci.* 41:1021-1026.
2. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopsisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. *Theor. Appl. Genet.* 103:415-424.
3. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for

linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.

4. Gaines, R.L., D.B. Bechtel, and Y. Pomeranz. 1985. A microscopic study on the development of a layer in barley that causes hull-caryopsis adherence. Cereal Chem. 62:35-40.

5. Hockett, E.A. 1981. Registration of hulless and hulless short-awned spring barley germplasm (Reg. nos. GP 35 to 52). Crop Sci. 21:146-147.

6. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.

7. Kikuchi, S., S. Taketa, M. Ichii, and S. Kawasaki. 2003. Efficient fine mapping of the naked caryopsis gene (*nud*) by HEGS (high efficiency genome scanning)/AFLP in barley. Theor. Appl. Genet. 108:73-78.

8. McGuire, C.F., and E.A. Hockett. 1981. Effect of awn length and naked caryopsis on malting quality of Betzes barley. Crop Sci. 21:18-21.

9. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] Bot. Mag., Tokyo 36:25-38. [In Japanese.]

10. Neatby, K.W. 1926. Inheritance of quantitative and other characters in a barley cross. Sci. Agric. 7:77-84.

11. Persson, G. 1969. An attempt to find suitable genetic markers for dense ear loci in barley I. Hereditas 62:25-96.

12. Robertson, D.W. 1937. Inheritance in barley. II. Genetics 22:443-451.

13. Scholz, F. 1955. Mutationsversuche an Kulturpflanzen. IV. Kulturpflanze 3:69-89.

14. So, M., S. Ogura, and Y. Imai. 1919. [A linkage group in barley.] Nogaku Kaiho 208:1093-1117. [In Japanese.]

15. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.

16. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.

17. Taketa, S., T. Awayama, S. Amano, Y. Sakurai, and M. Ichii. 2006. High-resolution mapping of the *nud* locus controlling the naked caryopsis in barley. Plant Breed. 125:337-342.

18. Taketa, S., S. Kikuchi, T. Awayama, S. Yamamoto, M. Ichii, and S. Kawasaki. 2004. Monophyletic origin of naked barley inferred from molecular analyses of a marker closely linked to the naked caryopsis gene (*nud*). Theor. Appl. Genet. 108:1236-1242.

19. Tschermak, E. von. 1901. Über Züchtung neuer Getreiderassen mittelst künstlicher Kreuzung. Kritisch-historische Betrachtungen. Zeitschrift für das landwirtschaftliche Versuchswesen Oesterreich 4:1029-1060.

20. Tsuchiya, T., and R.J. Singh. 1973. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 3:75-78.

21. Ubisch, G. von. 1921. Beitrag zu einer Faktorenanalyse von Gerste. III. Z. Indukt. Abstammungs. Vererbungsl. 25:198-200.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:110.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:51-52.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:195-196.

BGS 9, Dense spike 1, *dsp1*

Stock number: BGS 9  
 Locus name: Dense spike 1  
 Locus symbol: *dsp1*

Previous nomenclature and gene symbolization:

Dense spike = *l* (19, 22).  
 Lax spike = *L<sub>1</sub>* (9).  
 Short spike = *e* (21).

Inheritance:

Monofactorial recessive (1, 6, 22).  
 Located in chromosome 7HS (7, 9); about 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (18, 19); near molecular marker cMWG704 (11); located near the centromere (11, 20); near markers Bmag0359 and Bmag0321 (20); *dsp1.a* is associated with SNP markers 2\_0671 to 2\_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (2); *dsp1.ap*, *dsp1.aq*, *dsp1.ar*, and *dsp1.at* have in common from their donor parent Volla SNP markers 1\_0299 to 2\_0485 (positions 101.23 to 121.90 cM) in 7H bin 07 of the Bowman backcross-derived lines BW263 to BW266 (2); *dsp1.ae*, *dsp1.ag*, *dsp1.ah*, and *dsp1.af* (formerly called *Pyr.af*) have Haisa-type of SNP marker patterns in the region from 1\_0128 to 1\_0169 (positions 97.66 to 142.55 cM) in 7H bins 07 to 08 of the Bowman backcross-derived lines BW255, BW256, BW257, and BW654 (2); *dsp1.aa* (formerly *pyr.aa*), *dsp1.ac*, *dsp1.ay*, and *dsp1.az* (BW652, BW254, BW271, and BW272, respectively) originated from different cultivars, but retained SNP marker in the centromeric region of 7H identical to those of the Haisa-type (2); *dsp1.f* (formerly *Zeo.f*) is associated with SNP markers 1\_1098 to 1\_0303 (positions 68.46 to 120.92 cM) in 7H bin 07 of the Bowman backcross-derived line BW935 (2); *dsp1.a* with *nud1.a* and *fst3.c* is associated with SNP markers 2\_0671 to 2\_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (2), in 7H bin 07.

Description:

Spike length is reduced because rachis internode length is reduced to about 2/3 normal. The reduction in rachis internode length caused by the *dsp1.a* and *uzu1.a* (*uzu 1*) alleles is similar and additive (16, 19). In F<sub>2</sub> progenies, the *dsp1.a* gene has pleiotropic effects on coleoptile length, culm length, and grain size (16). The original mutant line for *dsp1.ah* (Mut. 4841) was associated with increased grain yield (12), but the Bowman backcross-derived line with *dsp1.ah* yielded less than half as much as Bowman (3). The rachis internode lengths of the Bowman backcross-derived lines from Volla mutants (BW263 to BW266) averaged 2.7 mm compared to 4.5 mm for Bowman. Plants were slightly shorter than Bowman, kernels were shorter 8.7 vs. 9.8 mm and slightly wider, and kernels weights were about 10% lower (5.2 vs. 5.7 mg). BW264, which contains only the 7H segment from Volla, appeared to have a lower reduction in plant height and kernel weights (3). The BW lines with the donor parents Haisa (BW255, BW654), Freya (BW256), and Saale (BW257) headed about two days later than Bowman and were about 20% shorter. Kernels were shorter and about 20% lighter. Awns of BW lines having Haisa-type as a donor were shorter, 9 vs. 11 cm, and grain yields were less than 50% of the Bowman yields. The Haisa line (BW654) retaining only a 7H region from the donor parent was later and shorter than the other Haisa-type lines (3). The BW lines with a Volla mutant differed from the BW lines with a Haisa mutant by only one SNP marker, 1\_1219 at 107.44 cM (3). Phenotypically, BW254 with *dsp1.ac*, BW271 with *dsp1.ay*, and BW272 with *dsp1.az* were similar to the BW lines from Volla, while BW652 with

*dsp1.aa* was similar to the BW lines from Haisa. Since BW lines from Haisa and Volla having other phenotypic variants have the same SNP marker heterogeneities in 7H lack the dense spike trait, the mutants named in this BGS description are likely independent mutants at the *dsp1* locus (2, 3). BW935 with *dsp1.f* was morphological similar to the BW lines with the Haisa mutants. The internode lengths in BW375 with *dsp1.a* were similar to those of other presumed *dsp1* mutants, but other morphological traits were affected by the presence of the *fst3.c* gene (3).

Origin of mutant:

Natural occurrence in cultivars from China, Japan, and Korea (22); X-ray induced mutants in Donaria and Haisa (13, 14); induced mutants in Haisa II (5).

Mutational events:

*dsp1.a* in many cultivars of Oriental origin, often associated with the short awn gene (16); *dsp1.f* (formerly called *Zeo.f*) (18:15:4l, GSHO 2137) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (8); *dsp1.aa* (formerly *pyr.aa*) (Betzes Erectoides, Clho 10871, GSHO 2431) in Betzes (PI 129430) (10); *dsp1.ac* (Mut. 2654, GSHO 1716) in Donaria (PI 161974) (13); *dsp1.ae* (Mut. 4014, GSHO 1717), *dsp1.af* (formerly *Pyr.af*) (Mut. 4158, GSHO 1718) in Haisa (PI 197617) (13), *dsp1.ag* (Mut. 4551, GSHO 1719) in Freya (PI 290197) (14), *dsp1.ah* (Mut. 4841) in Saale (Pirolina, PI 539132) (12); *dsp1.ap* (7112, GSHO 1724), *dsp1.aq* (7113, GSHO 1725), *dsp1.ar* (7114, GSHO 1726), *dsp1.at* (7117, GSHO 1727) in Volla (PI 280423) (4, 5); *dsp1.ay* (WA11005-81, GSHO 1729) in WA9037-75 (see PI 639908 for pedigree) (23); *dsp1.az* (Wa1628-85) in Hazen (PI 483238) (23).

Mutant used for description and seed stocks:

*dsp1.a* in Honen 6 (OUJ469, PI 307495, GSHO 1232); *dsp1.aa* (Betzes Erectoides, Clho 10871, GSHO 2431) in Betzes; *dsp1.ar* in Volla (GSHO 1726); *dsp1.f* in Bowman\*7 (GSHO 2137, BW935, NGB 22364); *dsp1.aa* in Bowman\*4 (GSHO 2236), in Bowman\*6 (BW652, NGB 22217); *dsp1.ac* in Bowman\*5 (GSHO 2237, BW254, NGB 22079); *dsp1.ae* in Bowman\*4 (GSHO 2239), in Bowman\*5 (BW255, NGB 22080); *dsp1.af* in Bowman\*5 (GSHO 2142) in Bowman\*6 (BW654, NGB 22219); *dsp1.ag* in Bowman\*4 (GSHO 2240), in Bowman\*5 (BW256, NGB 22081); *dsp1.ah* in Bowman\*7 (BW257, NGB 22082); *dsp1.ap* in Bowman\*4 GSHO 2245, in Bowman\*5 (BW263, NGB 22088); *dsp1.aq* in Bowman\*5 (GSHO 2246), in Bowman\*6 (BW264, NGB 22089); *dsp1.ar* in Bowman\*7 (GSHO 1942, BW265, NGB 22090); *dsp1.at* in Bowman\*5 (GSHO 2247, BW267, NGB 22092); *dsp1.ay* in Bowman\*3 (GSHO 2250, BW271, NGB 22096); *dsp1.az* in Bowman\*5 (BW272, NGB 22097); *dsp1.a* with *nud1.a* and *fst3.c* from Kobinkatagi 4 (OUM 382, GSHO 1746) in Bowman\*6 (GSHO 1842); *dsp1.a* with *nud1.a* and *fst3.c* in Bowman\*7 (BW375, NGB 20614).

References:

1. Biffen, R.H. 1907. The hybridization of barleys. III. J. Agric. Sci. 2:183-206.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Gaul, H.P.K. 1986. (Personal communications).
5. Gaul, H. 1964. Mutations in plant breeding. Rad. Bot. 4:155-232.
6. Hayes, H.K., and H.V. Harlan. 1920. The inheritance of the length of internode in the rachis of the barley spike. U. S. Dept. Agric., Bull. 869. 26 pp.
7. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
8. Lehmann, L.C. 1985. (Personal communications).
9. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] Bot. Mag., Tokyo 36:25-38. [In Japanese.]



10. Ramage, R.T. and G.A. Wiebe. (Unpublished, see <http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1053879>).
11. Sameri, M., K. Takeda, and T. Komatsuda. 2006. Quantitative trait loci controlling agronomic traits in recombinant inbred lines from a cross of oriental- and occidental-type barley cultivars. *Breed. Sci.* 56:243-252.
12. Scholz, F. 1971. Utilization of induced mutations in barley. Recent information of linkage and chromosome mapping. p. 94-105. *In* R.A. Nilan (ed.) *Barley Genetics II*. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
13. Scholz, F., and C. O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. I. Kulturpflanze 6:123-166.
14. Scholz, F., and C. O. Lehmann. 1959. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. III. Kulturpflanze 9:230-272.
15. Shahinnia, F., A. Druka, R. Waugh, M. Morgante, and N. Stein. 2010. Positional cloning of the gene dense spike (*dsp1*) on barley chromosome 7H by utilization of next generation grass-genomic tools. p. 319 (abstr.). *In* Proceed. Plant and Animal Genome XVIII Conference, 9 Jan. 2010, San Diego, USA.
16. Takahashi, R. 1951. Studies on the classification and geographic distribution of the Japanese barley varieties. II. Correlative inheritance of some quantitative characters with the ear type. *Ber. Ohara Inst. landw. Forsch.* 9:383-398.
17. Takahashi, R. 1987. Genetic features of East Asian barleys. pp. 7-20. *In* Yasuda, S., and T. Konishi (eds.) *Barley Genetics V*. Proc. Fifth Int. Barley Genetics Symp., Okayama, 1986. Sanyo Press Co. Okayama, Japan.
18. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. *Barley Genet. Newsl.* 5:56-60.
19. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. *Ber. Ohara Inst. landw. Forsch.* 10:29-52.
20. Taketa, S., T. Yuo, Y. Sakurai, S. Miyake, and M. Ichii. 2011. Molecular mapping of the short awn 2 (*lks2*) and dense spike 1 (*dsp1*) genes on barley chromosome 7H. *Breed. Sci.* 61: 80-85.
21. Takezaki, Y. 1927. [On the genetical formulae of the length of spikes and awns in barley, with reference to the computation of the valency of the heredity factors.] *Rep. Agric. Exp. Sta., Tokyo* 46:1-43. [In Japanese.]
22. Ubisch, G. von. 1916. Beitrag zu einer Faktorenanalyse von Gerste. *Z. Indukt. Abstammungs. Vererbungsl.* 17:120-152.
23. Ullrich, S.E., and A. Aydin. 1988. Mutation breeding for semi-dwarfism in barley. p. 135-144. *In* *Semi-dwarf Cereal Mutants and Their Use in Cross-breeding III*. IAEA-TECDOC-455. IAEA, Vienna.

Prepared:

R. Takahashi. 1972. *Barley Genet. Newsl.* 2:174.

Revised:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:53.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:63-65.

BGS 10, Short awn 2, *lks2*

Stock number: BGS 10  
Locus name: Short awn 2  
Locus symbol: *lks2*

Previous nomenclature and gene symbolization:

Short awn = *a* (22, 23).  
Short awn = *lk* (20).  
Short awn 2 = *lk<sub>1</sub>* (9).  
Short awn 2 = *lk2* (14).  
Short awn 4 = *lk4* (3, 7).

Inheritance:

Monofactorial recessive (8, 9, 17).  
Located in chromosome 7HL (8, 19); estimates ranged from 7.9 to 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (4, 17, 19); about 2.8 cM distal from molecular marker WG541 in 7H bin 05 (10); 3.6 cM from AFLP marker E4138-3 in subgroup 6 of the Proctor/Nudinka map (11); about 8.6 cM proximal from RFLP marker WG380B in 7H bin 08 (1); near EST-based marker k04151 and k06123 (21); *lks2.b* is associated with SNP markers 2\_0790 to 2\_0060 (positions 73.96 to 97.66 cM) in 7H bins 06 and 07 of the Bowman backcross-derived line BW492 (2), likely in 7H bin 07.

Description:

Awns of both central and lateral spikelets are reduced to about 3/5 of the long awned type. Texture of the short awn is finer and more flexible than that of the long awn, especially in non-uzu genotypes (19, 20). Kernel weights of *lks2* plants were slightly reduced and kernels per spike were slightly increased, but other traits remained unchanged (18). The Atlas near-isogenic lines for *lks2* (half awn) were found to respond better to environmental and genetic stress than the normal lines (15, 16). The awn length of heterozygotes in some crosses was shorter than that of the normal parent. Awns, as measured from the tip of the last fertile spikelet on the spike to the tip of the awn, of the Bowman backcross-derived line BW492 were about 1/2 as long as Bowman awns, 5 to 6 vs. 11 to 12 cm. Kernels of BW492 plants were slightly lighter than those of Bowman in some tests and kernel width was slightly less. Other agronomic traits were similar to those of Bowman (5).

Origin of mutant:

Spontaneous occurrence in some cultivars and distributed in China, Japan, Korea, and Nepal (7, 13, 17, 20).

Mutational events:

*lks2.b* in cultivars of Oriental origin, often associated with the *dsp1.a* (dense spike 1) gene (8, 17, 20); a possible mutant in Morex (CIho 15773) (12, 13).

Mutant used for description and seed stocks:

*lks2.b* (GSHO 566) in Honen 6 (OUJ469, PI 307495,) (20); *lks2.b* from Sermo (CIho 7776) in Betzes (PI 129430)\*7 (CIho 16558, GP 36), *lks2.b* from Sermo in Compana (CIho 5438)\*7 (CIho 16188, GP 40), *lks2.b* from Sermo in Decap (CIho 3351)\*7 (CIho 16562, GP 44) (6); *lks2.b* from R.I. Wolfe's Multiple Recessive Stock (GSHO 3451) in Bowman (PI 483237)\*9 (GSHO 1850, BW492, NGB 20720).

References:

1. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. *Theor. Appl. Genet.* 103:415-424.

2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Eslick, R.F., and E.A. Hockett. 1967. Allelism for awn length, *lk2*, in barley (*Hordeum* species). *Crop Sci.* 7:266-267.
4. Eslick, R.F., and E.A. Hockett. 1972. Recombination values of four genes on chromosome 1. *Barley Genet. Newsl.* 2:123-126.
5. Franckowiak, J.D. (Unpublished).
6. Hockett, E.A. 1981. Registration of hulless and hulless short-awned spring barley germplasm (Reg. nos. GP 35 to 52). *Crop Sci.* 21:146-147.
7. Litzenberger, S.C., and J.M. Green. 1951. Inheritance of awns in barley. *Agron. J.* 43:117-123.
8. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] *Bot. Mag., Tokyo* 36:25-38. [In Japanese.]
9. Myler, J.L. 1942. Awn inheritance in barley. *J. Agric. Res.* 65:405-412.
10. Pozzi, C., P. Faccioli, V. Terzi, A.M. Stanca, S. Cerioli, P. Castiglioni, R. Fink, R. Capone, K.J. Müller, G. Bossinger, W. Rohde, and F. Salamini. 2000. Genetics of mutations affecting the development of a barley floral bract. *Genetics* 154:1335-1346.
11. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.
12. Ramage, T. 1984. A semi-dominant short awn mutant in Morex. *Barley Genet. Newsl.* 14:19-20.
13. Ramage, T., and J.L.A. Eckhoff. 1985. Assignment of mutants in Morex to chromosomes. *Barley Genet. Newsl.* 15:22-25.
14. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. *J. Am. Soc. Agron.* 33:47-64.
15. Schaller, C.W., C.O. Qualset, and N. J. Rutger. 1972. Isogenic analysis of the effects of the awn on productivity of barley. *Crop Sci.* 12:531-535.
16. Schaller, C.W., and C.O. Qualset. 1975. Isogenic analysis of productivity in barley: Interaction of genes affecting awn length and leaf-spotting. *Crop Sci.* 15:378-382.
17. So, M., S. Ogura, and Y. Imai. 1919. [A linkage group in barley.] *Nogaku Kaiho* 208:1093-1117. [In Japanese.]
18. Takahashi, R. 1987. Genetic features of East Asian barleys. pp. 7-20. *In* S. Yasuda and T. Konishi (eds.) *Barley Genetics V. Proc. Fifth Int. Barley Genetics Symp.*, Okayama, 1986. Sanyo Press Co., Okayama.
19. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. *Barley Genet. Newsl.* 5:56-60.
20. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. *Ber. Ohara Inst. landw Forsch.* 10:29-52.
21. Taketa, S., T. Yuo, Y. Sakurai, S. Miyake, and M. Ichii. 2011. Molecular mapping of the short awn 2 (*lks2*) and dense spike 1 (*dsp1*) genes on barley chromosome 7H. *Breed. Sci.* 61: 80-85.
22. Takezaki, Y. 1927. [On the genetical formulae of the length of spikes and awns in barley, with reference to the computation of the valency of the heredity factors.] *Rep. Agric. Exp. Sta., Tokyo* 46:1-43. [In Japanese.]
23. Ubisch, G. von. 1921. Beitrag zu einer Faktorenanalyse von Gerste. III. *Z. Indukt. Abstammungs. Vererbungsl.* 25:198-200.

Prepared:

R. Takahashi. 1972. *Barley Genet. Newsl.* 2:176.

Revised:

- R. Takahashi and T. Tsuchiya. 1973. Barley Genet. Newsl. 3:119.  
J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:54-55.  
J.D. Franckowiak 2007. Barley Genet. Newsl. 37:197-198.  
J.D. Franckowiak 2011. Barley Genet. Newsl. 41:66-68.

BGS 11, Unbranched style 4, *ubs4*

Stock number: BGS 11  
Locus name: Unbranched style 4  
Locus symbol: *ubs4*

Previous nomenclature and gene symbolization:

Unbranched style 4 = *u4* (8).  
Breviaristatum-15 = *ari-15* (4).  
Breviaristatum-d = *ari-d* (2, 3, 4, 6).  
Short awn 8 = *lk8* (9).

Inheritance:

Monofactorial recessive (6, 8).  
Located in chromosome 7HL (6, 7, 8); about 8.0 cM distal from the *nud1* (naked caryopsis 1) locus (8); *ubs4.d* is associated with SNP markers 2\_0103 to 1\_0563 (positions 139.96 to 154.35 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW884 (1); *ari-d.15* is associated with SNP marker 1\_0169 (position 142.66 cM) in 7H bin 08 of the Bowman backcross-derived line BW041 (1); *ari-d.44* is associated with SNP markers 1\_0056 to 2\_0092 (positions 51.93 to 152.29 cM) in 7H bins 04 to 09 of the Bowman backcross-derived line BW035 (1), in 7H bin 08.

Description:

The stigma has only a few very short branches. This prevents normal pollen reception and reduces seed set to 13 to 30% in *uzu* type plants. Both the *uzu1.a* and *srh1.a* (short rachilla hair) genes interact with *ubs4.d* to further reduce in seed set. Pollen fertility is normal (8). Awn length is about 1/4 normal (4). Seed set on plants of the Bowman backcross-derived lines for *ari-d.15* and *ubs4.d*, BW041 and BW884, respectively, varied from about 10% for plants grown in greenhouses to nearly 50% for plants grown at Aberdeen, Idaho, USA (2). Awns of the Bowman backcross-derived-lines for *ubs4.d*, BW884, and *ari-d.15*, BW041, extended about 3 cm beyond the tip of the tip while those of Bowman extended about 11 cm (2). Grain yields of BW041 and BW884 ranged from 1/4 to 1/2 those of Bowman. Compared to Bowman, kernel weights varied from slightly less to slightly more. Other morphological traits were similar to those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Ao Hadaka (OUJ159) (8).

Mutational events:

*ubs4.d* (GSHO 567) in Ao Hadaka (Ao Hadaka-hen) (8); *ari-d.15* (NGB 115861, GSHO 1652), *-d.35* (NGB 115884), *-d.51* (NGB 115901) in Bonus (PI 189763) (4); *ari-d.44* (NGB 115891), *-d.57* (NGB 115911) in Bonus (5); *ari-d.105* (NGB 115917), *-d.107* (NGB 115919), *-d.116* (NGB 115928), *-d.129* (NGB 115940), *-d.130* (NGB 115941), *-d.150* (NGB 115961), *-d.160* (NGB 115970), *-d.186* (NGB 115996), *-d.187* (NGB 115997), *-d.192* (NGB 116002), *-d.193* (NGB 116003), *-d.232* (NGB 116042), *-d.239* (NGB 116048), *-d.240* (NGB 116049), *-d.241* (NGB 116050), *-d.242* (NGB 116051), *-d.243* (NGB 116052), *-d.247* (NGB 116058) in Foma (CIho 11333), *-d.288* (NGB 116105) in Kristina (NGB 1500) (4).

Mutant used for description and seed stocks:

*ubs4.d* in Ao Hadaka (GSHO 567); *ari-d.15* in Bonus (GSHO 1652, NGB 115861); *ubs4.d* in Bowman (PI 483237)\*6 (GSHO 1849); *ubs4.d* in Bowman\*7 (BW884, NGB 22318); *ari-d.15* in Bowman\*8 (GSHO 1848, BW041, NGB 20449); *ari-d.44* in Bowman\*6 (BW035, NGB 20443).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.

2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of brevistaristatum mutants in barley. *Hereditas* 80:263-278.
5. Lundqvist, U. (Unpublished).
6. Persson, G. 1969. An attempt to find suitable genetic markers for dense ear loci in barley I. *Hereditas* 62:25-96.
7. Persson, G., and A. Hagberg. 1965. Localization of nine induced mutations in the barley chromosomes. *Barley Newsl.* 8:52-54.
8. Takahashi, R., J. Yamamoto, and S. Yasuda. 1953. Inheritance of semi-sterility due to defects of stigmatic structure in barley. *Nogaku Kenkyu* 41:69-78. [In Japanese with English summary.]
9. Tsuchiya, T. 1974. Allelic relationships of genes for short-awned mutants in barley. *Barley Genet. Newsl.* 4:80-81.

Prepared:

R. Takahashi. 1972. *Barley Genet. Newsl.* 2:177.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:56.

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:69-70.

BGS 12, Desynapsis 1, *des1*

Stock number: BGS 12  
Locus name: Desynapsis 1  
Locus symbol: *des1*

Previous nomenclature and gene symbolization:

Long chromosome = *lc* (1, 6, 8).

Inheritance:

Monofactorial recessive (1, 6).

Located in chromosome 7H (1, 6); *des1.a* is associated with SNP markers 2\_1491 to 2\_0495 (positions 64.19 to 121.90 cM) in 7H bins 05 to 07 of the Bowman backcross-derived line BW228 (2); *des1.v* is associated with SNP markers 2\_0126 to 1\_0056 (positions 49.45 to 51.93) in 7H bin 04 of the Bowman backcross-derived line BW229 (2), likely in 7H bin 05.

Description:

The name long chromosome refers to the frequent occurrence of rod bivalents at metaphase I (3). The chromosomes are paired during pachytene, but undergo desynapsis during diplotene. The degree of desynapsis is  $d = 2.6 \pm 1.6$  ranged from 7 ring bivalents ( $d = 0$ ) to 5 rod bivalents plus 4 univalents ( $d = 9$ ). Lagging chromosomes and micronuclei were observed frequently at telophase I. Microspore tetrads contained an average of 0.3 micronuclei per tetrad with a range of 0 to 6. Ovule fertility was about 45% (4). Seed set on BW229, the Bowman backcross-derived line with the *des1.v* mutant, was variable with grain yields ranging from very little to 40% of the Bowman yields. BW229 plants headed 2 to 3 days later than Bowman and had about 4 more developed spikelets per spike. Kernels of BW229 weighed 5 to 10% more than Bowman kernels (3).

Origin of mutant:

An X-ray induced mutant in Mars (CIho 7015) (3, 6).

Mutational events:

*des1.a* (GSHO 592) in Mars (CIho 7015) (1, 6, 7); *des1.v* in Freja (CIho 7130) (5, 7).

Mutant used for description and seed stocks:

*des1.a* (GSHO 592) in Mars; *des1.a* in Bowman\*2 (BW228, NGB 22055); *des1.v* in Bowman\*6 (BW229, NGB 22056).

References:

1. Burnham, C.R. 1946. A gene for "long" chromosome in barley. Genetics 31:212-213. (Abstr.)
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Hernandez-Soriano, J.M. 1973. Desynaptic mutants in Betzes barley. M.S. Thesis. Univ. of Arizona, Tucson.
5. Hernandez-Soriano, J.M., and R.T. Ramage. 1973. Coordinator's report. Desynaptic genes. Barley Genet. Newsl. 3:91.
6. McLennan, H.A. 1947. Cytogenetic studies of a strain of barley with long chromosomes. M.S. Thesis. Univ. of Minnesota, St. Paul.
7. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. Barley Genet. Newsl. 2:65-68.
8. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.

Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:124.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:57.

J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:58-59.



BGS 13, Desynapsis 4, *des4*

Stock number: BGS 13  
Locus name: Desynapsis 4  
Locus symbol: *des4*

Previous nomenclature and gene symbolization:  
None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7H (1); *des4.af* is associated with SNP markers 1\_0772 to 2\_0790 (positions 71.81 to 73.96 cM) in 7H bin 05 and markers 2\_0311 to 2\_1448 (positions 126.28 to 134.43 cM) in 7H bin 08 of Bowman backcross-derived line BW240 (1); *des4.d* is associated with SNP markers 1\_838 to 2\_1201 (positions 49.53 to 134.43 cM) in 7H bins 04 to 08 of Bowman backcross-derived line BW241 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is  $d = 3.3 \pm 2.2$  with a range from 7 ring bivalents ( $d = 0$ ) to 3 rod bivalents plus 8 univalents ( $d = 11$ ). Many of the univalents split longitudinally during anaphase I, and lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore tetrads contained an average of 1.0 micronuclei per tetrad and the range was 0 to 10. Ovule fertility was about 18% (3). Plants of the Bowman backcross-derived line for *des4.af*, BW240, were similar to Bowman except grain yields were 25 to 50% lower. Kernels were about 10% lighter than those of Bowman in most trials (2).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (5, 6).

Mutational events:

*des4.d* (GSHO 595), *des4.h* in Betzes (5, 6); *des4.z*, *des4.aa*, *des4.ab*, *des4.ac*, *des4.ad*, *des4.ae*, *des4.af*, *des4.ag* in Klages (CIho 15487) (4, 7); all the Klages mutants may be identical because they were isolated from the same field (4).

Mutant used for description and seed stocks:

*des4.d* GSHO 595) in Betzes (, *des4.d* in Bowman\*5 (BW241, NGB 22068); *des4.af* in Bowman\*7 (BW240, NGB 22067).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hernandez-Soriano, J.M. 1973. Desynaptic mutants in Betzes barley. M.S. Thesis. Univ. of Arizona, Tucson.
4. Hernandez-Soriano, J.M., and R.T. Ramage. 1974. Coordinator's report. Desynaptic genes. *Barley Genet. Newsl.* 4:123-125.
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1971. Desynaptic genes in Betzes barley. *Barley Genet. Newsl.* 1:38.
6. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.
7. Scheuring, J.F., D.R. Clark, and R.T. Ramage. 1976. Coordinator's report: Desynaptic genes. *Barley Genet. Newsl.* 6:108-109.

Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. *Barley Genet. Newsl.*

3:127.

Revised:

R.T. Ramage and J.F. Scheuring. 1976. Barley Genet. Newsl. 6:116.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:58.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:71-72.

BGS 14, Desynapsis 5, *des5*

Stock number: BGS 14  
Locus name: Desynapsis 5  
Locus symbol: *des5*

Previous nomenclature and gene symbolization:  
None.

Inheritance:  
Monofactorial recessive (4, 5).  
Located in chromosome 7HL (4); *des5.e* is associated with SNP markers 2\_0139 to 2\_1363 (positions 194.97 to 198.70 cM) in 7H bin12 and with SNP markers 1\_1198 to 2\_1275 (positions 73.70 to 104.73) of the Bowman backcross-derived line BW244 (1), most likely in 7H bin 12.

Description:  
The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is  $11.1 \pm 2.6$  ranging from 7 ring bivalents ( $d = 0$ ) to 14 univalents ( $d = 14$ ). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 4.5 micronuclei per quartet with a range of 0 to 18. Ovule fertility is about 7%. When crossed with non-allelic desynaptic lines, the  $F_1$ 's frequently show a low degree of desynapsis (up to 3 rod bivalents per cell) (3). Plants of the Bowman backcross-derived line for *des5.e*, BW244, exhibited variable seed set with grain yields from 1/4 to 1/2 those of Bowman. Plant heights of BW244 ranged from 90% of Bowman to the same height and kernels weights were 80% of those for Bowman to almost the same (2).

Origin of mutant:  
A spontaneous mutant in Betzes (PI 129430) (4, 5).

Mutational events:  
*des5.e* (GSHO 596), *des5.f*, *des5.g* in Betzes (4, 5).

Mutant used for description and seed stocks:  
*des5.e* (GSHO 596) in Betzes; *des5.e* in Bowman\*4 (BW244, NGB 22070).

References:  
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.  
2. Franckowiak, J.D. (Unpublished).  
3. Hernandez-Soriano, J.M. 1973. Desynaptic mutants in Betzes barley. M.S. Thesis. Univ. of Arizona, Tucson.  
4. Ramage, R.T., and J.M. Hernandez-Soriano. 1971. Desynaptic genes in Betzes barley. *Barley Genet. Newsl.* 1:38.  
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.

Prepared:  
J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. *Barley Genet. Newsl.* 3:128.

Revised:  
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:59.  
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:73.

BGS 15, Non-blue aleurone xenia 1, *blx1*

Stock number: BGS 15  
Locus name: Non-blue aleurone xenia 1  
Locus symbol: *blx1*

Previous nomenclature and gene symbolization:

Blue aleurone = *Bl* (1).

Complementary factors for blue vs. white aleurone = *Bl1* and *bl1* (3).

Complementary factors for blue vs. white aleurone = *Blx* and *blx* (9).

Inheritance:

Monofactorial recessive (1, 3) when complementary dominant alleles are present at the *Blx2*, *Blx3*, *Blx4*, and *Blx5* loci (2).

Located in chromosome 4HL (1, 6, 7); over 13.6 cM distal from the *glf3* (glossy leaf 3) locus (8).

Description:

Blue aleurone color is due to anthocyanin pigments (5), which occur as lumps inside many aleurone granules in some or all aleurone cells (2). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (2, 3). Aleurone color is best observed in well-filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (4).

Origin of mutant:

Natural occurrence in many cultivars, frequently in those of Occidental origin.

Mutational events:

*blx1.a* (GSHO 185) in Goldfoil (PI 5975) (6).

Mutant used for description and seed stocks:

*blx1.a* (GSHO 185) in Goldfoil; the dominant allele is present in Bowman (PI 483237).

References:

1. Buckley, G.F.H. 1930. Inheritance in barley with special reference to the color of caryopsis and lemma. *Sci. Agric.* 10:460-492.
2. Finch, R. A., and E. Simpson. 1978. New colours and complementary colour genes in barley. *Z. Pflanzenzücht.* 81:40-53.
3. Kushnak, G.D. 1974. Utilizing linkages of genetic male sterile and aleurone color genes in hybrid barley (*Hordeum vulgare* L.) systems. Ph.D. Thesis. Montana State Univ., Bozeman.
4. Mullick, D.B., and V.C. Brink. 1970. A method for exposing aleurone tissue of barley for color classification. *Can. J. Plant Sci.* 50:551-558.
5. Mullick, D.B., D.G. Faris, V.C. Brink, and R.M. Acheson. 1958. Anthocyanins and anthocyanidins of the barley pericarp and aleurone tissues. *Can. J. Plant Sci.* 38:445-456.
6. Myler, J.L., and E.H. Stanford. 1942. Color inheritance in barley. *J. Am. Soc. Agron.* 34:427-436.
7. Robertson, D.W., G.W. Deming, and D. Koonce. 1932. Inheritance in barley. *J. Agric. Res.* 44:445-466.
8. Takahashi, R., J. Hayashi, and I. Moriya. 1971. Linkage studies in barley. *Barley Genet. Newsl.* 1:51-58.
9. Wiebe, G.A. 1972. Blue aleurone caused by complementary genes in very close translinkage. *Barley Genet. Newsl.* 2:109.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:111.

Revised:

R.A. Finch. 1978. Barley Genet. Newsl. 8:163.

J.D. Franckowiak and R.A. Finch. 1997. Barley Genet. Newsl. 26:60.

BGS 16, Waxy endosperm 1, *wax1*

Stock number: BGS 16  
Locus name: Waxy endosperm 1  
Locus symbol: *wax1*

Previous nomenclature and gene symbolization:

Waxy endosperm = *wx* (12).  
High amylopectin endosperm = *g/lx* (3, 8).

Inheritance:

Monofactorial recessive (5, 7).  
Located in chromosome 7HS (4, 11); about 1.5 cM proximal from the *fch12* (chlorina seedling 12) locus (12); about 12.6 cM proximal from the *Run1* (reaction to *Ustilago nuda* 1) locus (10); *wax1.a* is associated with SNP markers 2\_0303 to 1\_0451 (positions 0.0 to 41.79 cM) in 7H bins 01 to 03 of the Bowman backcross-derived line BW905 (1), likely in 7H bin 02.

Description:

The endosperm contains primarily amylopectin, chains of alpha- (164) D-glucopyranose units branched through alpha-(166) linkages, and has a waxy texture. The starch content is reduced, the amount of sucrose and maltose is increased significantly, and more amylopectin may be deposited (6). The starch in the endosperm and pollen grains has reddish-brown reaction to iodine (5, 7). The estimated spontaneous reversion to normal for six *wax1* alleles ranged from 1.9 to  $5.6 \times 10^{-5}$ , and the intralocus recombination frequencies ranged from 0.4 to  $194 \times 10^{-5}$  (8). Instability of the *wax1.a* allele from R.I. Wolfe's Multiple Recessive Stock is induced by crossing to mutant line 152 (9).

Origin of mutant:

A spontaneous mutant in Murasaki Mochi (CIho 5899) (5, 7).

Mutational events:

*wax1.a* (GSHO 84) in Murasaki Mochi (CIho 5899) (5, 7); *wax1.b*, *wax1.c*, *wax1.d*, *wax1.e*, *wax1.f*, and *wax1.g* in Steptoe (CIho 15229) (3, 8).

Mutant used for description and seed stocks:

*wax1.a* in Oderbrucker (CIho 4666)\*10 (Waxy Oderbrucker, CIho 7563, GSHO 908); *wax1.a* from R.I. Wolfe's Multiple Recessive Stock in Bowman (PI 483237)\*8 (GSHO 1828, BW905, NGB 22336).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Kleinhofs, A., R.L. Warner, F.J. Muelbauer, and R.A. Nilan. 1978. Induction and selection of specific gene mutations in *Hordeum* and *Pisum*. *Mutat. Res.* 51:29-35.
4. Kramer, H.H., and B.A. Blander. 1961. Orientating linkage maps on the chromosomes of barley. *Crop Sci.* 1:339-342.
5. Nakao, S. 1950. On waxy barleys in Japan. *Seiken Zihō* 4:111-113. [In Japanese with English summary.]
6. Newman, C.W., and R.K. Newman. 1992. Nutritional aspects of barley seed structure and composition. p. 351-368. *In* P.R. Shewry (ed.) *Barley: Genetics, Biochemistry, Molecular Biology, and Biotechnology*. (Biotechnology in Agriculture no. 5). CAB International, Wallingford, UK.
7. Ono, T., and H. Suzuki. 1957. Endosperm characters in hybrids between barley varieties with starchy and waxy endosperms. *Seiken Zihō* 8:11-19.

8. Rosichan, R.A., P. Arenaz, and A. Kleinhofs. 1979. Intragenic recombination at the *waxy* locus in *Hordeum vulgare*. Barley Genet. Newsl. 9:79-85.
9. Schreiber, H., and A. Habekuß. 1996. High frequencies of forward and reverse genetic changes at the *waxy*-locus of barley (*Hordeum vulgare* L.). Barley Genet. Newsl. 25:41-45.
10. Shands, R.G. 1964. Inheritance and linkage to stem rust and loose smut resistance and starch type in barley. Phytopathology 54:308-316.
11. Shapter, F.M., P. Egger, L.S. Lee, and R.J. Henry. 2009. Variation in Granule Bound Starch Synthase I (GBSSI) loci amongst Australian wild cereal relatives (Poaceae). J. Cereal Sci. 49:4-11.
12. Tabata, M. 1961. Studies of a gametophyte factor in barley. Jpn. J. Genet. 36:157-167.
13. Webster, O.J. 1950. Genetics and morphology of rachis internode length. Ph.D. Thesis. Univ. of Minnesota, St. Paul.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:97.

Revised:

T. Tsuchiya. 1982. Barley Genet. Newsl. 12:109.

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:61-62.

J.D. Franckowiak 2012. Barley Genet. Newsl. 42:65-66.

BGS 17, Chlorina seedling 4, *fch4*

Stock number: BGS 17  
Locus name: Chlorina seedling 4  
Locus symbol: *fch4*

Previous nomenclature and gene symbolization:

Chlorina seedling 4 = *f4* (3, 6).

Yellow viable = *yv* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 7HL (1, 2, 5, 6); slightly distal from the *nud1* (naked caryopsis 1) locus (1); about 4.4 cM proximal from the *lks2* (short awn 2) locus (1).

Description:

Seedlings are bright yellow-green on emergence and maintain this color until they are nearly mature. Seedlings and plants are relatively vigorous, but heading is delayed (6).

Origin of mutant:

A beta-ray induced mutant in Montcalm (CIho 7149) (6).

Mutational events:

*fch4.g* (Alb Acc 258, GSHO 1214) in Montcalm (CIho 7149) (6).

Mutant used for description and seed stocks:

*fch4.g* (GSHO 1214) in Montcalm; *fch4.g* in Bowman (PI 483237)\*7 (GSHO 1851, BW360, NGB 20599).

References:

1. Eslick, R.F. 1976. Approximate position of the chlorina mutants *f4f4* and *f8f8* on chromosome 1. Barley Genet. Newsl. 6:10-13.
2. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.
3. Robertson, D.W. 1964. New genes in barley with their relation to linkage groups and chromosomes. p. 159-180. In S. Broekhuizen, G. Dantuma, H. Lamberts, and W. Lange (eds.) Barley Genetics I. Proc. First Int. Barley Genet. Symp., Wageningen, 1963. Centre for Agricultural Publications and Documentation, Wageningen.
4. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III, 1954-1963. Crop Sci. 5:33-43.
5. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. Barley Genet. Newsl. 2:93-98.
6. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:98.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:103.

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:63.



BGS 18, Chlorina seedling 5, *fch5*

Stock number: BGS 18  
Locus name: Chlorina seedling 5  
Locus symbol: *fch5*

Previous nomenclature and gene symbolization:

Chlorina seedling 5 = *f5* (4).

Yellow viable = *yv2* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HS (1, 3, 4); proximal from the *brh1* (brachytic 1) locus (1); about 25.9 cM proximal from the *Rpg1* (reaction to *Puccinia graminis tritici* 1) locus (2).

Description:

Seedlings are pale yellow to ivory in color at emergence and remain this color until they are nearly mature (4). Seedlings are relatively weak and rarely survive to maturity in the field at Fargo, North Dakota, USA; however, in the greenhouse they gradually become darker green and produce late-maturing plants.

Origin of mutant:

A spontaneous mutant in Gateway (CIho 10072) (4).

Mutational events:

*fch5.f* (GSHO 1215, Alb Acc 328) in Gateway (CIho 10072) (4).

Mutant used for description and seed stocks:

*fch5.f* (GSHO 1215) in Gateway; *fch5.f* in Bowman (PI 483237)\*5 (GSHO 1827); *fch5.f* in Bowman\*7 (BW361, NGB 20600).

References:

1. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. *Can. J. Genet. Cytol.* 14:949-957.
2. Jin, Y., B.J. Steffenson, and J.D. Franckowiak. 1993. Linkage between the *Rpg1* gene for stem rust resistance and the *f5* locus on barley chromosome 1. *Crop Sci.* 33:642-643.
3. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. *Barley Genet. Newsl.* 2:93-98.
4. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. *Can. J. Genet. Cytol.* 5:200-219.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:99.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:64.

BGS 19, Non-blue aleurone xenia 2, *blx2*

Stock number: BGS 19  
Locus name: Non-blue aleurone xenia 2  
Locus symbol: *blx2*

Previous nomenclature and gene symbolization:

Blue aleurone 1 = *Bl*<sub>1</sub>, a second factor for blue aleurone (5).  
Non-blue aleurone 2 = *bl*<sub>2</sub> (6).

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1*, *Blx3*, *Blx4*, and *Blx5* loci (1, 2).  
Located in chromosome 7HL (1, 2); approximately 9.9 cM distal from the *nud1* (naked caryopsis 1) locus (5).

Description:

Blue aleurone color is due to anthocyanin pigments (4), which occur as lumps inside many aleurone granules in some or all aleurone cells (1). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (1, 2). Aleurone color is best observed in well-filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (3).

Origin of mutant:

Natural occurrence in some cultivars of Oriental origin.

Mutational events:

*blx2.b* in Nepal (CIho 595, GSHO 209) (5).

Mutant used for description and seed stocks:

*blx2.b* (GSHO 209) in Nepal; *blx2.b* is likely present in Bowman (PI 483237); wild type *Blx2* from Aohadaka-hen (see OUJ159) in Bowman\*5 (GSHO 2022); *Blx2* from ICARDA Green (GSHO 1564) in Bowman\*6 (BW063, NGB 20471).

References:

1. Finch, R.A., and E. Simpson. 1978. New colours and complementary colour genes in barley. *Z. Pflanzenzücht.* 81:40-53.
2. Kushnak, G.D. 1974. Utilizing linkages of genetic male sterile and aleurone color genes in hybrid barley (*Hordeum vulgare* L.) systems. Ph.D. Thesis. Montana State Univ., Bozeman.
3. Mullick, D.B., and V.C. Brink. 1970. A method for exposing aleurone tissue of barley for color classification. *Can. J. Plant Sci.* 50:551-558.
4. Mullick, D.B., D.G. Faris, V.C. Brink, and R.M. Acheson. 1958. Anthocyanins and anthocyanidins of the barley pericarp and aleurone tissues. *Can. J. Plant Sci.* 38:445-456.
5. Myler, J.L., and E.H. Stanford. 1942. Color inheritance in barley. *J. Am. Soc. Agron.* 34:427-436.
6. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. *J. Am. Soc. Agron.* 39:464-473.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:100.

Revised:

R.A. Finch. 1978. *Barley Genet. Newsl.* 8:164.  
J.D. Franckowiak and R.A. Finch. 1997. *Barley Genet. Newsl.* 26:65.

BGS 20, Reaction to barley yellow mosaic virus 2, *Rym2*

Stock number: BGS 20  
Locus name: Reaction to barley yellow mosaic virus 2 (BaYMV)  
Locus symbol: *Rym2*

Previous nomenclature and gene symbolization:

Resistance to BaYMV 2 = *Ym2* (4).

Inheritance:

Monofactorial incomplete dominant (4).

Located in chromosome 7HL (4); approximately 31.4 cM distal from the *nud1* (naked caryopsis 1) locus (4).

Description:

Plants with *Rym2.b* allele have much less yellowing and stunting than susceptible plants when grown in fields that are infested with BaYMV (2). Also, Mihori Hadaka 3 is resistant to BaYMV, BaYMV-2, and BaMMV in Germany (1, 2).

Origin of mutant:

Natural occurrence in Mihori Hadaka 3 (OUJ373, PI 467403) (4), and other cultivars of Oriental origin (2, 3).

Mutational events:

*Rym2.b* in Mihori Hadaka 3 (PI 467403) (4).

Mutant used for description and seed stocks:

*Rym2.b* in Mihori Hadaka 3 (OUJ373, PI 467403, GSHO 984).

References:

1. Götz, R., and W. Friedt. 1993. Mode of inheritance and genetic diversity of BaMMV resistance of exotic barley germplasms carrying genes different from '*ym4*'. Theor. Appl. Genet. 86:229-233.
2. Orden, F., and W. Friedt. 1993. Resistance to the barley yellow mosaic virus complex — Different genotypic reactions and genetics of BaMMV-resistance of barley (*Hordeum vulgare* L.). Plant Breed. 111:125-131.
3. Orden, F., R. Götz, and W. Friedt. 1993. Genetic stocks resistant to barley mosaic viruses (BaMMV, BaYMV, BaYMV-2) in Germany. Barley Genet. Newsl. 22:46-50.
4. Takahashi, R., I. Hayashi, T. Inouye, I. Moriya, and C. Hirao. 1973. Studies on resistance to yellow mosaic disease in barley. I. Tests for varietal reaction and genetic analysis of resistance to the disease. Ber. Ohara Inst. landw. Biol., Okayama Univ. 16:1-17.

Prepared:

R.G. Timian. 1976. Barley Genet. Newsl. 6:117.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:66.

BGS 21, Reaction to *Ustilago nuda* 1, *Run1*

Stock number: BGS 21  
Locus name: Reaction to *Ustilago nuda* 1 (loose smut)  
Locus symbol: *Run1*

Previous nomenclature and gene symbolization:

Resistance to *Ustilago nuda* = *Un* (3).

Inheritance:

Monofactorial dominant (2, 6).

Located in chromosome 7HS (1, 5); about 2.0 cM proximal from the *Rpg1* (reaction to *Puccinia graminis* 1) locus (1, 5); about 12.7 cM distal from the *wax1* (waxy endosperm 1) locus (1, 5); about 15.1 cM distal from the *nud1* (naked caryopsis 1) locus (8).

Description:

Plants have a dominant gene, which controls a resistant reaction to "non-Trebi-attacking" cultures of *Ustilago nuda* and to cultures capable of infecting the "Jet" type of resistance (7).

Origin of mutant:

Natural occurrence in Trebi (PI 537442) (2, 4).

Mutational events:

*Run1.a* in Trebi (PI 537442, GSHO 1324) (4, 5, 7).

Mutant used for description and seed stocks:

*Run1.a* in Trebi (GSHO 1324).

References:

1. Andrews, J.E. 1956. Inheritance of reaction to loose smut, *Ustilago nuda*, and to stem rust, *Puccinia graminis tritici*, in barley. Can. J. Agric. Sci. 36:356-370.
2. Livingston, J.E. 1942. The inheritance of resistance to *Ustilago nuda*. Phytopathology 32:451-466.
3. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.
4. Schaller, C.W. 1949. Inheritance of resistance to loose smut, *Ustilago nuda*, in barley. Phytopathology 39:959-979.
5. Shands, R.G. 1964. Inheritance and linkage to stem rust and loose smut resistance and starch type in barley. Phytopathology 54:308-316.
6. Skoropad, W.P., and P.V. Johnson. 1952. Inheritance of resistance to *Ustilago nuda* in barley. Can. J. Bot. 30:525-536.
7. Thomas, P.L. 1974. The occurrence of loose smut of barley on commercially grown cultivars possessing genes for resistance from Jet. Can. J. Plant Sci. 54:453-456.
8. Wells, S.A. 1958. Inheritance of reaction to *Ustilago hordei* (Pers. Lagerh.) in cultivated barley. Can. J. Plant Sci. 38:45-60.

Prepared:

D.R. Metcalfe and P.L. Thomas. 1976. Barley Genet. Newsl. 6:118.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:67.

BGS 22, Reaction to *Schizaphis graminum* 1, *Rsg1*

Stock number: BGS 22  
Locus name: Reaction to *Schizaphis graminum* 1 (greenbug)  
Locus symbol: *Rsg1*

Previous nomenclature and gene symbolization:

Greenbug resistance = *Grb* (8).

Resistance to *Schizaphis graminum* Rondani (greenbug) = *Rsg<sub>1</sub>.a* (3).

Inheritance:

Monofactorial dominant (2, 3, 9).

Located in chromosome 7H (4).

Description:

Resistant seedlings infested with greenbugs (aphids) are not killed, while susceptible seedlings are killed, eight weeks after infestation by the buildup of the greenbug population (2, 3, 4). The resistance provided by Post 90 (PI 549081), having the *Rsg1.a* gene, to most *S. graminum* biotypes was commonly 2 to 3 readings on a 1 to 9 scale (7). Accessions with the *Rsg1.a* gene conferred resistance to most, but not all greenbug populations (5).

Origin of mutant:

Natural occurrence in Bozu Omugi (OUJ028, PI 87181), Derbent (PI 76504), and Kearney (PI 539126, CIho 7580) (1, 3).

Mutational events:

*Rsg1.a* in Bozu Omugi (PI 87181), Derbent (PI 76504), Kearney (PI 539126, CIho 7580), Dobaku (PI 87817), and CIho 5087 (PI 82683) (3, 7).

Mutant used for description and seed stocks:

*Rsg1.a* in Bozu Omugi (GSHO 1317, PI 87181); *Rsg1.a* in Post 90 (PI 549081) from Will (CIho 11652) (5).

References:

1. Atkins, I.M., and R.G. Dahms. 1945. Reaction of small-grain varieties to greenbug attack. USDA Tech. Bull. 901.
2. Gardenshire, J.H. 1965. Inheritance and linkage studies on greenbug resistance in barley (*Hordeum vulgare* L.). Crop Sci. 5:28-29.
3. Gardenshire, J.H., and H.L. Chada. 1961. Inheritance of greenbug resistance in barley. Crop Sci. 1:349-352.
4. Gardenshire, J.H., N.A. Tuleen, and K.W. Stewart. 1973. Trisomic analysis of greenbug resistance in barley, *Hordeum vulgare* L. Crop Sci. 13:684-685.
5. Mornhinweg, D.W., L.H. Edwards, L.H. Smith, G.H. Morgan, J.A. Webster, D.R. Porter, and B.F. Carver. 2004. Registration of 'Post 90' barley. Crop Sci. 44:2263.
6. Porter, D.R., J.D. Burd, and D.W. Mornhinweg. 2007. Differentiating greenbug resistance genes in barley. Euphytica 153:11-14.
7. Porter, D.R., and D.W. Mornhinweg. 2004. Characterization of greenbug resistance in barley. Plant Breed. 123:493-494.
8. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1955. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement II, 1947-1953. Agron. J. 47:418-425.
9. Smith, O.D., A.M. Schlehuber, and B.C. Curtis. 1962. Inheritance studies of greenbug (*Toxoptera graminum* Rond.) resistance in four varieties of winter barley. Crop Sci. 2:489-491.

Prepared:

J.G. Moseman. 1976. Barley Genet. Newsl. 6:119.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:68.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:199-200.

BGS 23, Winding dwarf 1, *wnd1*

Stock number: BGS 23  
Locus name: Winding dwarf 1  
Locus symbol: *wnd1*

Previous nomenclature and gene symbolization:  
None.

Inheritance:  
Monofactorial recessive (1).  
Located in chromosome 4HL (1); *wnd1.a* is associated with SNP markers 1\_1398 to 2\_0384 (positions 127.80 to 133.98 cM) in 4H bins 09 to 10 of the Bowman backcross-derived line BW906 (1). Previously located in chromosome 7HS (3); over 25.4 cM distal from the *dsp1* (dense spike 1) locus (3).

Description:  
Plants are semidwarf (15 cm shorter than the original cultivar) and have a pronounced coiling or winding of the upper portion of peduncle (3). The original stock for the *wnd1.a* gene also contained the dense spike (*dsp1.a*) gene, but the Bowman backcross-derived line, BW906, does not (2). Only a slight and inconsistent reduction in plant height was observed in BW906 compared to Bowman. However, the BW906 plants had a distinct coiling of the upper portion of the peduncle. No other morphological differences compared to Bowman were observed (2).

Origin of mutant:  
A gamma-ray induced mutant in Kogen-mugi (OUJ099, PI 383956) from M Toda (3).

Mutational events:  
*wnd1.a* (OUM309, GSHO 2499, G754) in Kogen-mugi (G754, OUJ099, PI 383956) (3).

Mutant used for description and seed stocks:  
*wnd1.a* in Kogen-mugi (OUM309, GSHO 2499); *wnd1.a* in Bowman (PI 483237)\*7 (GSHO 1832, BW906, NGB 22337).

References:  
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.  
2. Franckowiak, J.D. (Unpublished).  
3. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. *Barley Genet. Newsl.* 5:56-60.

Prepared:  
J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:69.

Revised:  
J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:74.

BGS 24, Fragile stem 3, *fst3*

Stock number: BGS 24  
Locus name: Fragile stem 3  
Locus symbol: *fst3*

Previous nomenclature and gene symbolization:

Fragile stem 3 = *fs3* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HS (1, 5); probably proximal from the *dsp1* (dense spike 1) locus based on linkage drag (4); *fst3.c* with *dsp1.a* and *nud1.a* is associated with SNP markers 2\_0671 to 2\_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (1), in 7H bin 07.

Description:

The leaf and stem characteristics of *fst3* plants are similar to those of *fst1* plants. Leaves and stems are very fragile and easily broken when slightly bent (5). Plants are about 2/3 normal height when protected in the greenhouse, but in the field plants are weak and are easily damaged by wind. The dense spike 1 (*dsp1.a*) and the naked caryopsis 1 (*nud1.a*) genes are also present with the *fst3.c* gene in Bowman backcross-derived line BW375 (3). BW375 plants were about half the height of Bowman, heading was delayed 3 to 10 days, kernels weight were 30 to 40% lower, and grain yields were from 0 to 30% of those for Bowman (3). In the OUM382 mutant line, crystalline cellulose content was reduced by 25% to 50% compared with the OUJ066 wild-type line (1, 6, 7, 8), and these reductions were similar to those observed in the *fst2* mutant lines (1, 8). The number of cellulose synthesizing terminal complexes was reduced by 80% in the *fst3.c* mutant (6).

Origin of mutant:

A spontaneous mutant in Kobinkatagi 4 (OUJ066, PI 190757) (5).

Mutational events:

*fst3.c* (OUM382, GSHO 1746) in Kobinkatagi 4 (OUJ066, PI 190757) (5).

Mutant used for description and seed stocks:

*fst3.c* (GSHO 1746, OUM382) in Kobinkatagi 4; *fst3.c* with *dsp1.a* and *nud1.a* in Bowman (PI 483237)\*5 (GSHO 1842); *fst3.c* with *dsp1.a* and *nud1.a* in Bowman\*7 (BW375, NGB 20614).

References:

1. Burton, R.A., G. Ma, U. Baumann, A.J. Harvey, N.J. Shirley, J. Taylor, F. Pettolino, A. Bacic, M. Beatty, C.R. Simmons, K.S. Dhugga, J.A. Rafalski, S.V. Tingey, and G.B. Fincher. 2010. A customized gene expression microarray reveals that the brittle stem phenotype *fs2* of barley is attributable to a retroelement in the HvCesA4 Cellulose Synthase Gene 1. *Plant Physiol.* 153:1716-1728.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
5. Hayashi, J., and I. Moriya. 1985. Trisomic analysis of a fragile stem mutant found in Kobinkatagi 4. *Barley Genet. Newsl.* 15:47-48.
6. Kimura, S., N. Sakurai, and T. Itoh. 1999. Different distribution of cellulose synthesizing complexes in brittle and non-brittle strains of barley. *Plant Cell Physiol.* 40:335-338.



7. Kokubo, A., S. Kuraishi, and N. Sakurai. 1989. Culm strength of barley: correlation among maximum bending stress, cell wall dimensions, and cellulose content. *Plant Physiol.* 91:876-882.

8. Kokubo, A., N. Sakurai, S. Kuraishi, K. Takeda. 1991. Culm brittleness of barley (*Hordeum vulgare* L.) mutants is caused by smaller number of cellulose molecules in cell wall. *Plant Physiol.* 97:509-514.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:70.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:74-75.

BGS 25, Xantha seedling 1, *Xnt1*

Stock number: BGS 25  
Locus name: Xantha seedling 1  
Locus symbol: *Xnt1*

Previous nomenclature and gene symbolization:

Xantha a =  $X_a$  (1).

Inheritance:

Monofactorial incomplete dominant (1).

Located in chromosome 7HL (1); over 35.9 cM distal from the *lks2* (short awn 2) locus (1, 4).

Description:

Segregation is observed each generation for xantha, chlorina, and green seedlings, but only the last two classes survive to maturity. Chlorina plants have a slightly yellow-green color until near maturity. Crosses to chlorina plants produce chlorina and green  $F_1$  plants in a 1:1 ratio. In the progeny of chlorina plants, xantha, chlorina, and green plants occur in a 1:2:1 ratio (1). Color differences between normal and heterozygous plants are observed in the *Xnt1.a2* mutant only prior to heading (3). Mutants at the *Xnt1* locus must be maintained as heterozygous stocks.

Origin of mutant:

An ethyl methanesulfonate induced mutant in the cross Akashinriki (OUJ659, PI 467400) X linkage tester 191 (OUL094) (1).

Mutational events:

*Xnt1.a* in the hybrid Akashinriki X linkage tester 191 (OUM215) (1, 4); *Xnt1.a2* in translocation stock T6-7d (3); *Xnt1.a3* in MC 20 (PI 357319) (2).

Mutant used for description and seed stocks:

*Xnt1.a* in the hybrid Akashinriki X linkage tester 191 (GSHO 1606); *Xnt1.a* in Bowman (PI 483237)\*7 (GSHO 1862, BW919, NGB 20790).

References:

1. Konishi, T. 1972. An incomplete dominant chlorophyll mutation on chromosome 1. Barley Genet. Newsl. 2:43-45.
2. Prina, A.R., M. del C. Arias, and M.C. de la Fuente. 1996. A new mutant allele for  $Xa/xa$  gene and its use for location of newly induced mutants in the long arm of barley's chromosome 1. Barley Genet. Newsl. 25:31-33.
3. Prina, A.R., and E.A. Favret. 1988. Influence of marker genes on the expression of somatic mutations. J. Hered. 79:371-376.
4. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1972. Inheritance and linkage studies in barley. V. Locating seven new mutant genes. Ber. Ohara Inst. landw. Biol., Okayama Univ. 15:147-168.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:71.

BGS 26, Subnodal bract 1, *snb1*

Stock number: BGS 26  
Locus name: Subnodal bract 1  
Locus symbol: *snb1*

Previous nomenclature and gene symbolization:

Subnodal bract = *sb* (2, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS (1, 3); near the centromere (1); about 36.3 cM proximal from the *brh1* (brachytic 1) locus (3).

Description:

A glume-like or stick-like bract arises immediately under the node-base (below and between the outer glumes) of the central spikelets. The bracts are present at only a few internodes on randomly arranged central spikelets. Not all spikes on affected plants have the extra bract (3).

Origin of mutant:

Natural occurrence in L50-220 (*Hordeum sativum* var *ibericum* from Russia) (3).

Mutational events:

*snb1.a* (GSHO 1217) in L50-200 (Alb Acc 67A) (2, 3), a recessive allele at the *brh1* locus is present in this stock also (3).

Mutant used for description and seed stocks:

*snb1.a* (GSHO 1217) in L50-200.

References:

1. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.
2. Walker, G.W., K. Kasha, and R.A. Miller. 1958. Recombination studies in barley. Proc. Genet. Soc. Can. 3:41-43.
3. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:72.

BGS 27, Long basal rachis internode 3, *lbi3*

Stock number: BGS 27  
Locus name: Long basal rachis internode 3  
Locus symbol: *lbi3*

Previous nomenclature and gene symbolization:

Long basal rachis internode 3 = *lb3* (1).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 7HL (3); over 20.0 cM distal from the *nud1* (naked caryopsis 1) locus (3); *lbi3.c* is associated with SNP markers 1\_0534 to 2\_0042 (positions 111.21 to 118.80) in 7H bin 07 of the Bowman backcross-derived line BW473 (1), in 7H bin 07.

Description:

Mutant plants in the cultivar Montcalm have a marked elongation and weakness of the basal rachis internode of the spike. This region may be 10 to 13 cm long in some tillers. The spike hangs vertically downward from the collar on emergence from the sheath and is often broken off in this region by the wind. When not broken off, spikes have normal fertility, contain well-filled grain, and show normal maturity (3). Expression of the *lbi3.c* allele in the Bowman-derived line is limited to a slight elongation of the basal rachis internode and a slightly lax spike.

Origin of mutant:

A gamma-ray induced mutant in Montcalm (CIho 7149) (3).

Mutational events:

*lbi3.c* (Alb Acc 291, GSHO 536), *lbi3.d* (Alb Acc 292), *lbi3.e* (Alb Acc 293), *lbi3.m* (Alb Acc 290) in Montcalm (CIho 7149) (3).

Mutant used for description and seed stocks:

*lbi3.c* (GSHO 536) in Montcalm; *lbi3.c* in Bowman (PI 483237)\*7 (GSHO 1840, BW473, NGB 20703).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. *Can. J. Genet. Cytol.* 2:397-415.

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:73.

Revised:

J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:79.

BGS 28, Erectoides-a, *ert-a*

Stock number: BGS 28  
Locus name: Erectoides-a  
Locus symbol: *ert-a*

Previous nomenclature and gene symbolization:

Erectoides-6 = *ert-6* (3).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HS (4, 10, 11); about 11.4 cM distal from the *cer-f* (eceriferum-f) locus (8, 9, 12, 13, 14); about 11.7 cM distal from the *nud1* (naked caryopsis 1) locus (8, 9, 11); *ert-a.6* is associated with SNP markers 1\_0394 to 2\_0103 (positions 107.44 to 142.55 cM) in 7H bins 07 to 08 of the Bowman backcross-derived line BW303 (1), likely in 7H bin 07, but in the long arm.

Description:

Spikes of all alleles have a compact appearance caused by a reduction in rachis internode length, with rachis internode length values from 1.7 to 2.6 mm (11). The *ert-a.6* allele produces plants with shorter internodes than most other *ert-a* alleles. Plants with an allele at the *ert-a* locus are 10 to 15 cm shorter than parental cultivars (6). The effects of the *ert-a* mutant on spike density are partially reversed by GA<sub>3</sub> treatments (15, 16). Plants of the Bowman backcross-derived line with *ert-a.6*, BW303, headed slightly earlier than Bowman and were about 15% shorter. Rachis internode lengths were 2.7 vs. 4.5 mm and kernel lengths averaged 8.8 vs. 9.9 mm. The kernel weights for BW303 were about 10% less than those for Bowman and grain yields were up to 25% less than those of Bowman (2). Based on phenotypic traits SNP markers from Gull retained in BW303, *ert-a.6* may be allele at the dense spike 1 (*dsp1*) locus (2).

Origin of mutant:

An X-ray induced mutant in Gull (CIho 1145, GSHO 466) (5, 6).

Mutational events:

*ert-a.6* (NGB 112609, GSHO 468), *-a.11* (NGB 112609) in Gull, *-a.13* (NGB 112614, GSHO 215) in Maja (PI 184884), *-a.19* (NGB 112621) *-a.21* (NGB 112622), *-a.21* (trans) (NGB 112623), *-a.23* (NGB 112624), *-a.28* (NGB 112628) in Bonus (PI 189763) (2, 3, 6), *-a.29* (NGB 112629) in Maja (6); *ert-a.36* (NGB 112637), *-a.38* (NGB 112638), *-a.49* (NGB 112648) in Bonus (4, 5); *ert-a.77* (NGB 112676) in Bonus (5); *ert-a.99* (NGB 112698) in Bonus (7); *ert-a.131* (NGB 112730), *-a.147* (NGB 112746), *-a.160h* (NGB 112759) in Bonus (11); *ert-a.160l* (NGB 112760), *-a.161* (NGB 112761) in Bonus (7); *ert-a.166* (NGB 112766) in Bonus, *-a.315* (NGB 112830), *-a.316* (NGB 112831) in Foma (CIho 11333) (11); *ert-a.323* (NGB 112838) in Foma (7); *ert-a.334* (NGB 112849), *-a.340b* (NGB 112856), *-a.341* (NGB 112857), *-a.343* (NGB 112859) in Foma (11); *ert-a.348* (NGB 112864) in Foma (7); *ert-a.350* (NGB 112866), *-a.364* (NGB 112880), *-a.368* (NGB 112834), *-a.378* (NGB 112894), *-a.388* (NGB 112903), *-a.406* (NGB 112922), *-a.433* (NGB 112949), *-a.481* (NGB 112997), *-a.494* (NGB 113010) in Foma (11); *ert-a.1180* (NGB 114058), *-a.1187* (NGB 114066), *-a.1193* (NGB 114072), *-a.1197* (NGB 114076), *-a.1203* (NGB 114082), *-a.1210* (NGB 114090), *-a.1219* (NGB 114099) in Bonus (7).

Mutant used for description and seed stocks:

*ert-a.6* in Gull (GSHO 468, NGB 112609); *ert-a.6* in Bowman (PI 483237)\*8 (GSHO 1844, BW303, NGB 20585).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development.. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å. 1947. Mutations in agricultural plants. Hereditas 33:1-100.
4. Hagberg, A. 1958. Cytogenetik einiger Gerstenmutanten. Züchter 28:32-36.
5. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
6. Hagberg, A., N. Nybom, and Å. Gustafsson. 1952. Allelism of *erectoides* mutations in barley. Hereditas 38:510-512.
7. Lundqvist, U. (Unpublished).
8. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. Hereditas 62:25-96.
9. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley II. Hereditas 63:1-28.
10. Persson, G., and A. Hagberg. 1962. Linkage studies with the erectoides loci. Barley Newsl. 5:46-47.
11. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
12. Søggaard, B. 1971. Linkage studies on eceriferum mutants in barley. Barley Genet. Newsl. 1:41-47.
13. Søggaard, B. 1974. The localization of *eceriferum* loci in barley. III. Three point tests of genes on chromosome 1 in barley. Hereditas 76:41-48.
14. Søggaard, B. 1977. The localization of eceriferum loci in barley. V. Three point tests of genes on chromosome 1 and 3. Carlsberg Res. Commun. 42:67-75.
15. Stoy, V., and A. Hagberg. 1958. Effects of gibberellic acid on erectoides mutations in barley. Hereditas 44:516-522.
16. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:74-75.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:76-77.

BGS 29, Erectoides-d, *ert-d*

Stock number: BGS 29  
Locus name: Erectoides-d  
Locus symbol: *ert-d*

Previous nomenclature and gene symbolization:

Erectoides-7 = *ert-7* (4).

Inheritance:

Monofactorial recessive (4, 5, 13).

Located in chromosome 7HS (1, 6, 13, 14); near the *ert-a* (erectoides-a) locus (11, 12); about 4.5 cM distal from the *cer-f* (eceriferum-f) locus (15, 16, 17); *ert-d.7* is associated with SNP markers 1\_0056 and 1\_0576 (positions 51.93 to 54.30 cM) in 7H bin 04, with SNP markers 2\_1338 and 1\_0823 (positions 65.93 to 173.82 cM) in 2H bins 06 to 09 and with SNP markers 2\_0193 and 1\_1503 (positions 65.93 to 173.82 cM) in 3H bins 05 to 12 of the Bowman backcross-derived line BW306 (2). The *ert-d* locus is likely in 7H bin 04, but a 2HL/3HL translocation is required for full expression (2, 3).

Description:

Spikes have a compact or semicompact appearance caused by a reduction in rachis internode length, with rachis internode length values from 1.5 to 1.8 mm for mutants of group one and 2.1 to 2.7 mm for mutants in group two (14). Plants with an allele at the *ert-d* locus can be placed in two plant height groups, but mutants with compact spikes are not all in the short plant height group (14). The *ert-d.7* allele is in group two based on rachis internode length and is closely linked to the translocation point (9). Rachis internode length increases following GA<sub>3</sub> treatment of plants that have alleles at the *ert-d* locus (18).

Origin of mutant:

An X-ray induced mutant in Gull (CIho 1145, GSHO 466) (8).

Mutational events:

*ert-d.7* (trans) (NGB 112610, GSHO 475) in Gull (CIho 1145, GSHO 466) (4, 8); *ert-d.14* (NGB 112616), *-d.15* (NGB 112617), *-d.30h* (NGB 112630, GSHO 476), *-d.30l* (NGB 112631) in Maja (PI 184884) (5, 6); *ert-d.33* (NGB 112634), *-d.43* (NGB 112643), *-d.60* (NGB 112659) in Bonus (PI 189763) (6); *ert-d.73* (NGB 112672) in Bonus (12); *ert-d.89* (NGB 112686) in Bonus (7); *ert-d.96* (NGB 112695), *-d.100* (NGB 112699), *-d.123* (trans) (NGB 112722, *-d.129* (NGB 112728), *-d.152* (NGB 112751), *-d.158* (NGB 112757) in Bonus, *-d.307* (NGB 112823), *-d.322* (NGB 112837), *-d.335* (NGB 112850), *-d.338* (NGB 112853), *-d.339* (NGB 112854), *-d.372* (NGB 112888), *-d.375* (NGB 112891), *-d.385a* (NGB 112900) in Foma (CIho 11333) (14); *ert-d.404* (NGB 112920) in Foma (10); *ert-d.405* (NGB 112921), *-d.420* (NGB 112936) in Foma (14).

Mutant used for description and seed stocks:

*ert-d.7* (GSHO 475, NGB 112610) in Gull; *ert-d.7* in Bowman (PI 483237)\*7 (GSHO 1845, BW306, NGB 20588).

References:

1. Burnham, C. R., and A. Hagberg. 1956. Cytogenetic notes on chromosomal interchanges in barley. *Hereditas* 42:467-482.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Gustafsson, Å. 1947. Mutations in agricultural plants. *Hereditas* 33:1-100.
5. Hagberg, A. 1954. Cytogenetic analysis of erectoides mutations in barley. *Acta Agric.*

Scand. 4:472-490.

6. Hagberg, A. 1958. Cytogenetik einiger Gerstenmutanten. Züchter 28:32-36.
7. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
8. Hagberg, A., N. Nybom, and Å. Gustafsson. 1952. Allelism of *erectoides* mutations in barley. Hereditas 38:510-512.
9. Hagberg, A., and J. H. Tjio. 1950. Cytological localization of the translocation point for the barley mutant *erectoides* 7. Hereditas 36:487-491.
10. Lundqvist, U. (Unpublished).
11. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. Hereditas 62:25-96.
12. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley II. Hereditas 63:1-28.
13. Persson, G., and A. Hagberg. 1962. Linkage studies with the *erectoides* loci. Barley Newsl. 5:46-47.
14. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
15. Søggaard, B. 1971. Linkage studies on *eceriferum* mutants in barley. Barley Genet. Newsl. 1:41-47.
16. Søggaard, B. 1974. The localization of *eceriferum* loci in barley. III. Three point tests of genes on chromosome 1 in barley. Hereditas 76:41-48.
17. Søggaard, B. 1977. The localization of *eceriferum* loci in barley. V. Three point tests of genes on chromosome 1 and 3. Carlsberg Res. Commun. 42:67-75.
18. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:76-77.

Revised:

U. Lundqvist and J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:82-83.



BGS 30, Erectoides-m, *ert-m*

Stock number: BGS 30  
Locus name: Erectoides-m  
Locus symbol: *ert-m*

Previous nomenclature and gene symbolization:

Erectoides-34 = *ert-34* (1, 2).

Inheritance:

Monofactorial recessive (1, 2, 8).

Located in chromosome 7HS (4, 5, 6, 8); about 14.7 cM distal from the *cer-f* (eceriferum-f) locus (9, 10, 11); near the *ant1* (anthocyanin-less 1) locus (8).

Description:

Spikes have a compact appearance caused by a reduction in rachis internode length, with rachis internode length values from 2.0 to 2.8 mm. However, the rachis internodes within each spike are often variable in length, and the spike appears irregular similar to those of opposite spikelet mutants. Plants with an allele at the *ert-m* locus are often 10 to 15 cm shorter than parental cultivars, and some tillers of most plants have one or more extremely shortened upper internodes (8). Alleles at the *ert-m* locus respond positively to GA<sub>3</sub> treatments designed to increase rachis internode length (12). Some alleles at the *ert-m* locus lack normal anthocyanin pigmentation. The anthocyanin deficiency can not be separated from the *ert-m* allele and is apparently an allele at the *ant1* locus (7, 8).

Origin of mutant:

A thermal neutron induced mutant in Bonus (PI 189763) (2, 8).

Mutational events:

*ert-m.34* (NGB 112635, GSHO 487), *-m.35* (NGB 112636), *-m.40* (NGB 112640), *-m.41* (NGB 112641), *-m.42* (NGB 112642), *-m.54* (NGB 112653), *-m.64* (NGB 112663) in Bonus (PI 189763) (2); *ert-m.87* (NGB 112687), *-m.107* (NGB 112706), *-m.115* (NGB 112714), *-m.130* (NGB 112729), *-m.144* (NGB 112743), *-m.168* (NGB 112768), *-m.169* (NGB 112769) in Bonus, *-m.314* (NGB 112829) in Foma (CIho 11333) (8); *ert-m.328* (NGB 112843) in Foma (3); *ert-m.330* (NGB 112845), *-m.363* (NGB 112879), *-m.384* (NGB 112899), *-m.426* (NGB 112942) in Foma (8).

Mutant used for description and seed stocks:

*ert-m.34* (NGB 112635, GSHO 487) in Bonus; *ert-m.34* in Bowman (PI 483237)\*8 (GSHO 1843, BW316, NGB 22111).

References:

1. Hagberg, A. 1958. Cytogenetik einiger Gerstenmutanten. Züchter 28:32-36.
2. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
3. Lundqvist, U. (unpublished).
4. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. Hereditas 62:25-96.
5. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley II. Hereditas 63:1-28.
6. Persson, G., and A. Hagberg. 1962. Linkage studies with the erectoides loci. Barley Newsl. 5:46-47.
7. Persson, G., and A. Hagberg. 1964. Linkage data from studies on mutations induced in Bonus barley. Barley Newsl. 7:39-41.
8. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
9. Søgaaard, B. 1971. Linkage studies on eceriferum mutants in barley. Barley Genet.

News. 1:41-47.

10. Søgaaard, B. 1974. The localization of *eceriferum* loci in barley. III. Three point tests of genes on chromosome 1 in barley. Hereditas 76:41-48.

11. Søgaaard, B. 1977. The localization of *eceriferum* loci in barley. V. Three point tests of genes on chromosome 1 and 3. Carlsberg Res. Commun. 42:67-75.

12. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. News. 26:78-79.

BGS 31, Shrunkendosperm xenia 6, *sex6*

Stock number: BGS 31  
Locus name: Shrunkendosperm xenia 6  
Locus symbol: *sex6*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 7HS (3); about 2.8 cM distal from the *seg2* (shrunkendosperm genetic 2) locus (2); about 3.1 cM from the centromere (3); over 45.8 cM proximal from the *Est5* (esterase 5) locus (3).

Description:

After the hard dough stage, kernels develop a depression in the center of the lemma, which becomes progressively more distinct with maturity. The depression is similar in size to that produced by *sex1* (shrunkendosperm xenia 1) mutants. The mutant has a xenia expression that permitting classification of kernels from heterozygous plants as normal or shrunkendosperm with an expected 3:1 ratio. Field establishment and growth of mutant plants is normal.

Origin of mutant:

A spontaneous mutant in K6827 (an introduction from Turkey) (1).

Mutational events:

*sex6.h* (GSHO 2476) in K6827 (MK6827) (1).

Mutant used for description and seed stocks:

*sex6.h* (GSHO 2476) in K6827, *sex6.h* in Bowman (PI 483237)\*6 (GSHO 3425); *sex6.h* in Bowman\*7 (BW846, NGB 22283).

References:

1. Biyashev, R.M., V.P. Netsvetaev, and A.A. Sozinov. 1986. Genetic control of some morphological markers for qualitative and biochemical characters and location of three genetic factors on chromosomes 1 and 5 of barley, *Hordeum vulgare* L. Sov. Genet. 22:226-232. (Translation of Genetika 22:296-303).
2. Netsvetaev, V.P. 1990. [Location of a shrunkendosperm gene, *sex 6*, in barley.] Nauchno-Tekh. Bull' VSGL, Odessa. No. 1 (75):31-35. [In Russian.]
3. Netsvetaev, V.P. 1992. [Use of double ditelosomics for gene location in barley.] Cytology and Genetics (Kiev) 26:26-30. [In Russian.]
4. Netsvetaev, V.P., and I.S. Krestinkov. 1993. Chromosomal position of the superoxide dismutase locus, *Sod1* (=Sod B), in barley. Barley Genet. Newsl.22:44-45.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl.26:80.

BGS 32, Reaction to *Puccinia hordei* 9, *Rph9*

Stock number: BGS 32  
Locus name: Reaction to *Puccinia hordei* 9 (barley leaf rust)  
Locus symbol: *Rph9*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 9 = *Pa*<sub>9</sub> (3, 7, 8).  
Resistance to *Puccinia hordei* Otth 9 = *Pa*9 (2).  
Resistance to *Puccinia hordei* 12 = *Rph*12 (1, 2, 9).

Inheritance:

Monofactorial dominant (1, 5, 6).  
Located in chromosome 5HL (5); about 26.1 cM distal from the *raw1* (smooth awn 1) locus (5); in 5H bin 11 about 9.3 cM proximal from esterase 9 (*Est*9) and about 22.5 cM proximal from STS marker ABC155 (1); about 29.2 cM distal from the *var1* (variegated 1) locus (1).

Description:

Seedling reaction types range from 0; or necrotic fleck to 23- or reduced pustule size (4, 6), but 0; reactions are more common with the *Rph9.z* allele, formerly *Rph*12.z (1, 2, 5). The resistant reaction of the *Rph9.i* allele is temperature sensitive and is inactivated above 20°C (3). Heterozygotes show an intermediate reaction to pathogenic isolates of *Puccinia hordei* (5). The original cultivar 'Trumpf' was also marketed in the United Kingdom as 'Triumph'.

Origin of mutant:

Natural occurrence in Abyssinian (Hor 2596, Clho 1234) (3, 7); natural occurrence in *Hordeum vulgare* subsp. *spontaneum*, but transferred to the cultivar Trumpf (Triumph, PI 548762, GSHO 1590) (2, 9).

Mutational events:

*Rph9.i* in Abyssinian (Hor 2596, Clho 1234) (3, 7); *Rph9.z* in Trumpf (PI 548762, GSHO 1590) (2, 9).

Mutant used for description and seed stocks:

*Rph9.i* in Abyssinian (GSHO 1601); *Rph9.i* in Bowman (PI 483237)\*8 (GSHO 1866, PI 643158, BW760, NGB 22466); *Rph9.z* in Trumpf (GSHO 1590); *Rph9.z* in Bowman\*4 (GSHO 2145); *Rph9.z* in Bowman \*8 (PI 643161); *Rph9.z* in Bowman\*9 (BW761, NGB 22467).

References:

1. Borovkova, I.G., Y. Jin, and B.J. Steffenson. 1998. Chromosomal location and genetic relationship of leaf rust resistance genes *Rph9* and *Rph12* in barley. *Phytopathology* 88:76-80.
2. Clifford, B.C. 1985. Barley leaf rust. p. 173-205. In W.R. Bushnell and A.P. Roelfs (eds.) *The Cereal Rusts*, Vol. II. Academic Press, New York.
3. Clifford, B.C., and A.C.C. Udeogalanya. 1976. Hypersensitive resistance of barley to brown rust (*Puccinia hordei* Otth). p. 27-29. In *Proc. 4th Eur. Medit. Cereal Rusts Conf.*, Interlaken, Switzerland.
4. Golan, T., Y. Anikster, J.G. Moseman, and I. Wahl. 1978. A new virulent strain of *Puccinia hordei*. *Euphytica* 27:185-189.
5. Jin, Y., G.D. Stadler, J.D. Franckowiak, and B.J. Steffenson. 1993. Linkage between leaf rust resistance genes and morphological markers in barley. *Phytopathology* 83:230-233.
6. Reinhold, M., and E.L. Sharp. 1982. Virulence types of *Puccinia hordei* from North America, North Africa and the Middle East. *Plant. Dis.* 66:1009-1011.

7. Tan, B.H. 1977. A new gene for resistance to *Puccinia hordei* in certain Ethiopian barleys. Cereal Rust Bull. 5:39-43.
8. Udeogalanya, A.C.C., and B.C. Clifford. 1976. Genetical, physiological and pathological relationships of resistance to *Puccinia hordei* and *P. striiformis* in *Hordeum vulgare*. Trans. Br. Mycol. Soc. 71:279-287.
9. Walther, U. 1987. Inheritance of resistance to *Puccinia hordei* Otth in the spring barley variety Trumpf. Cereal Rusts Powdery Mildews Bull. 15:20-26.

Prepared:

- J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:81.  
J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:281 as BGS 333, Reaction to *Puccinia hordei* 12, *Rph12*.

Revised:

- J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:201-202.

BGS 33, Anthocyanin-less 1, *ant1*

Stock number: BGS 33  
Locus name: Anthocyanin-less 1  
Locus symbol: *ant1*

Previous nomenclature and gene symbolization:

Green stem = *rs* (1).  
Exrubrum-a = *rub-a* (5).

Inheritance:

Monofactorial recessive (1, 6).  
Located in chromosome 7HS (1); near the centromere (3); near the *ert-m* (erectoides-m) locus (8); about 15.0 cM distal from the *nud11* (naked caryopsis 1) locus (1); *Rst1.a* is associated with SNP markers 2\_0074 to 2\_0113 (positions 71.81 to 75.21 cM) in 7H bin 05 of the Bowman backcross-derived line BW762 (2); *ant1.1* is associated with SNP markers 1\_0838 to 2\_0103 (positions 49.53 to 139.86 cM) in 7H bins 04 to 08 of the Bowman backcross-derived line BW013 (2), in 7H bin 05.

Description:

When grown under favorable light conditions, red pigmentation of the stem does not occur (1). Anthocyanin pigments are not observed in the stem, auricles, awns, or lemma veins of induced *ant1* mutants (4). However, moderate to strong pigmentation of these plant parts is observed in plants homozygous for the normal allele *Rst1.a* at this locus. The *ant1.b* allele, which occurs frequently in cultivars of Manchurian origin and is present in Bowman (PI 483237), reduces considerably the red pigmentation of stem, auricles, awns, and lemma veins. Expression of alleles at the *ant1* locus is easier to observe at the stem base of seedlings.

Origin of mutant:

Natural occurrence in some cultivars, frequently in those of Oriental origin (4); an alpha ray induced mutant in Bonus (PI 189763) (6).

Mutational events:

*ant1.b* (*rst1.b*) in Manchurian introductions (4); *ant1.1* (NGB 114552), *ant1.2* (NGB 114553), *ant1.4* (NGB 114555) in Bonus (PI 189763) (6); *ant1.56* in Bonus (7).

Mutant used for description and seed stocks:

*ant1.1* (GSHO 1620, NGB 114552) in Bonus; *ant1.1* from Bonus in Bowman (PI 483237)\*3 (BW013, NGB 20421); *Rst1.a* in Goldfoil (PI 5975, GSHO 185) (1, 3); *ant1.b* from six-rowed Manchurian type cultivars is in Bowman (4); *Rst1.a* from Mut. 4128 of Haisa (PI 197617) in Bowman\*6 (GSHO 1834); *Rst1.a* from Mut. 4128 in Bowman\*7 (BW762, NGB 22230).

References:

1. Briggs, F.N., and E.H. Stanford. 1943. Linkage relations of the Goldfoil factor for resistance to mildew in barley. J. Agric. Res. 66:1-5.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.
4. Franckowiak, J.D. (Unpublished).
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
6. Jende-Strid, B., and U. Lundqvist. 1978. Diallelic tests of anthocyanin-deficient mutants. Barley Gent. Newsl. 8:57-59.

7. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. Barley Gent. Newsl. 14:76-79.

8. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:

T.E. Haus. 1975. Barley Gent. Newsl. 5:96 as BGS 15, Red stem, *Rs*.

Revised:

J.D. Franckowiak. 1997. Barley Gent. Newsl. 26:82.

J.D. Franckowiak. 2012. Barley Gent. Newsl. 42:89-90.

BGS 34, Male sterile genetic 50, *msg50*

Stock number: BGS 34  
Locus name: Male sterile genetic 50  
Locus symbol: *msg50*

Previous nomenclature and gene symbolization:

Male sterile genetic hm = *msg*, *hm* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 7HL (1); about 13.6 cM from the *lks2* (short awn 2) locus (1).

Description:

Selfing - 0% is reported (3), but occasionally 5 to 10% selfed seed set is observed.

Outcrossing - complete female fertility (3).

Stamens - anthers slightly smaller than fertile sib with filament elongation and stomium (3).

Origin of mutant:

A spontaneous mutant in Maris Mink (PI 467824) (3).

Mutational events:

*msg50.gh* (MSS435) in Maris Mink (PI 467824) (1, 3); *msg50.hm* (MSS466, GSHO 2404) in Berac (PI 355136) (1, 3).

Mutant used for description and seed stocks:

*msg50.hm* (GSHO 2404) in Berac; *msg50.hm* in Bowman (PI 483237)\*7 (GSHO 1861, BW588, NGB 23448); *msg50.gh* from MSS435 in Bowman\*4 (BW972, NGB 23467).

References:

1. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. *Barley Genet. Newsl.* 20:31-36.
2. Franckowiak, J.D. 1993. Identification of two additional loci that control genetic male sterility in barley. *Barley Genet. Newsl.* 22:10-11.
3. Hockett, E. A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:83.



BGS 35, Reaction to barley stripe mosaic virus 1, *rsm1*

Stock number: BGS 35  
Locus name: Reaction to barley stripe mosaic virus 1 (BSMV)  
Locus symbol: *rsm1*

Previous nomenclature and gene symbolization:

Resistance to barley stripe mosaic virus = *sm* (2).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HS (1, 4); over 24.3 cM distal from the *nud1* (naked caryopsis 1) locus (4); over 28.2 cM from the *lks2* (short awn 2) locus (4); cosegregation with RFLP marker ABC455 (1).

Description:

Reaction to BSMV is estimated as the frequency or percentage of plants infected following inoculation of barley seedlings with a specific strain of BSMV. Highly resistant cultivars produce few or no infected plants 7 to 14 days after inoculation. Most or all seedlings of highly susceptible cultivars produce broad mosaic stripes within 7 days after inoculation (3). Several genes control reaction to BSMV and show additive inheritance patterns (2, 5). The study of progeny from crosses between resistant and moderately susceptible cultivars indicates that one recessive factor controls the frequency of infected plants (1, 4). This gene for reaction to BSMV is assigned the gene symbol *rsm1.a*.

Origin of mutant:

Natural occurrence in Modjo 1 (CIho 14048) and Moreval (PI 95258) (2, 5).

Mutational events:

*rsm1.a* in Modjo 1 (2, 4, 5).

Mutant used for description and seed stocks:

*rsm1.a* in Modjo 1; *rsm1.a* in Morex (CIho 15773, GSHO 2492) (1); *rsm1.a* is present in Bowman (PI 483237).

References:

1. Edwards, M.C., and B.J. Steffenson. 1996. Genetics and mapping of barley stripe mosaic virus resistance in barley. *Phytopathology* 86:184-187.
2. Sisler, W.W., and R.G. Timian. 1956. Inheritance of barley stripe mosaic resistance in Modjo (C.I. 3212) and C.I. 3212-1. *Plant. Dis. Rep.* 40:1106-1107.
3. Timian, R.G. 1974. The range of symbiosis of barley and barley stripe mosaic virus. *Phytopathology* 64:342-345.
4. Timian, R.G., and J.D. Franckowiak. 1987. Location of a factor for barley stripe mosaic virus reaction on chromosome 1. *Barley Genet. Newsl.* 17:79-82.
5. Vasquez, G.G., G.A. Peterson, and R.G. Timian. 1974. Inheritance of barley stripe mosaic reaction in crosses among three barley varieties. *Crop Sci.* 14:429-432.

Prepared:

J.D. Franckowiak and M.C. Edwards. 1997. *Barley Genet. Newsl.* 26:84.

BGS 36, Xantha seedling 4, *xnt4*

Stock number: BGS 36  
Locus name: Xantha seedling 4  
Locus symbol: *xnt4*

Previous nomenclature and gene symbolization:

Yellow seedling (2).  
Xantha seedling c2 =  $x_{c2}$  (3).

Inheritance:

Monofactorial recessive (2).  
Located in chromosome 7HL (1); over 22.0 cM from the centromere using the translocation stock T1-6a as a tester (1).

Description:

Seedlings have a yellow color and die at a two to three leaf stage (2). The *xnt4.d* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Coast (PI 539103) (2).

Mutational events:

*xnt4.d* ( $x_{c2}$ ) (Coast I, GSHO 42) in Coast (PI 539103) (2).

Mutant used for description and seed stocks:

*xnt4.d* (GSHO 42) in Coast.

References:

1. Kramer, H.H., and B.A. Swomley Blander. 1961. Orienting linkage maps on the chromosomes of barley. Crop Sci. 1:339-342.
2. Robertson, D.W., and G.W. Deming. 1930. Genetic studies in barley. J. Hered. 21:283-288.
3. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:85.

BGS 37, Xantha seedling 9, *xnt9*

Stock number: BGS 37  
Locus name: Xantha seedling 9  
Locus symbol: *xnt9*

Previous nomenclature and gene symbolization:

Albino seedling d = *alb,,d* (1).

Xantha seedling i = *xan,,i* (2).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 7HL (2); over 7.4 cM from the *msg23* (male sterile genetic 23) locus (2).

Description:

Seedlings have a yellow color and die at the two to three leaf stage (1). The *xnt9.i* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Erbet (CIho 13826) (1).

Mutational events:

*xnt9.i* (GSHO 584) in Erbet (CIho 13826) (1).

Mutant used for description and seed stocks:

*xnt9.i* (GSHO 584) in Erbet.

References:

1. Rahman, M.M. 1973. Balanced male sterile-lethals systems for hybrid barley production. Ph.D. Thesis. Montana State Univ., Bozeman.
2. Rahman, M.M., and R.F. Eslick. 1976. Linkage of spontaneous mutant seedling lethal genes with genetic male sterile genes. Barley Genet. Newsl. 6:53-58.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:86.

BGS 38, Seminudoides 1, *smn1*

Stock number: BGS 38  
Locus name: Seminudoides 1  
Locus symbol: *smn1*

Previous nomenclature and gene symbolization:

Seminuoides = *smn* (3, 4).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HS (2); based on linkage drag with the *ant1* (anthocyanin-less 1) locus (2).

Description:

The caryopsis of *smn1* plants is not completely covered because gaps develop between the margins of the lemma and palea. Adherence of the lemma and the palea to the pericarp is poor, but the grain does not thresh free from the hull at maturity. Tiller number and grain yield are often reduced (1, 4).

Origin of mutant:

An X-ray induced mutant in Haisa (PI 197617) (3, 4).

Mutational events:

*smn1.a* (Mut. 4128, GSHO 1602) in Haisa (PI 197617) (4).

Mutant used for description and seed stocks:

*smn1.a* (Mut. 4128, GSHO 1602) in Haisa; *smn1.a* in Bowman (PI 483237)\*5 (GSHO 3420, BW871, NGB20786).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
3. Scholz, F. 1956. Mutationsversuche an Kulturpflanzen. V. Die Vererbung zweier sich variabel manifestierender Übergangsmerkmale von bespelzter zu nackter Gerste bei röntgeninduzierten Mutanten. Kulturpflanze 4:228-246.
4. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l.l. Kulturpflanze 6:123-166.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. Barley Genet. Newsl. 32:78.

BGS 39, Midseason stripe 2, *mss2*

Stock number: BGS 39  
Locus name: Midseason stripe 2  
Locus symbol: *mss2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS (2); based on linkage drag with the *Lga1* (Long glume awn 1) and *dsp1* (dense spike 1) loci (2, 3).

Description:

A variable number of broad, white stripes develop in tillers during the joining stage. Leaves and spikes show white sectors that persist until maturity. Expression of *mss2* is temperature dependent with few or no stripes developing in cool environments and numerous white stripes in warm environments. When numerous stripes develop, spike length, and plant vigor are reduced (1).

Origin of mutant:

A spontaneous mutant in breeding line ND11258 (Bowman\*2/ND7556) (1).

Mutational events:

*mss2.b* (GSHO 2409) in ND11258 (2).

Mutant used for description and seed stocks:

*mss2.b* (GSHO 2409) in ND11258; *mss2.b* in Bowman (PI 483237)\*7 (GSHO 2148, BW594, NGB 22160).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
3. Kleinhofs, A. 1999. Coordinator's report: Integrating barley molecular and morphological/physiological marker maps. Barley Genet. Newsl. 29:58-59.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:79.

BGS 40, Premature ripe 1, *prm1*

Stock number: BGS 40  
Locus name: Premature ripe 1  
Locus symbol: *prm1*

Previous nomenclature and gene symbolization:

Premature ripe = *pmr* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS (3); based on linkage drag with the *Lga1* (long glume awn 1) locus (3); near the centromere (5, 6).

Description:

The *prm1* gene induces plants to start dying about two weeks after heading. Seedlings are slightly pale green in color and plants are shorter than normal sibs. The lighter shade of green persists until senescence of the plants begins. Premature dying is associated with rapid collapse of the straw and very thin grain (2).

Origin of mutant:

A sodium azide induced mutant in Glenn (Clho 15769) (1).

Mutational events:

*prm1.a* (DWS1069, GSHO 2429) in Glenn (Clho 15769) (4).

Mutant used for description and seed stocks:

*prm1.a* (GSHO 2429) in Glenn, *prm1.a* in Bowman (PI 483237)\*7 (GSHO 3434, BW645, NGB 22210).

References:

1. Faue, A.C. 1987. Chemical mutagenesis as a breeding tool for barley. M.S. Thesis. North Dakota State Univ., Fargo.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Kleinhofs, A. 1997. Integrating barley RFLP and classical marker maps. Barley Genet. Newsl. 27:105-112.
6. Kudrna, D., A. Kleinhofs, A. Kilian, and J. Soule. 1996. Integrating visual markers with the Steptoe x Morex RFLP map. Vol. 1. p. 343. In A.E. Slinkard, G.J. Scoles, and B.G. Rossmagel (eds.). Barley Genetics VII. Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp., Saskatoon. Univ. Ext. Press, Univ. of Saskatchewan, Saskatoon, Canada.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:80.

BGS 41, Brachytic 7, *brh7*

Stock number: BGS 41  
Locus name: Brachytic 7  
Locus symbol: *brh7*

Previous nomenclature and gene symbolization:

Brachytic-w = *brh.w* (4).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 7H (2); *brh7.w* is associated with SNP markers 1\_0299 to 1\_0169 (positions 101.23 to 142.55 cM) in 7H bins 07 to 08 of the Bowman backcross-derived line BW099 (2). Previously located in chromosome 5HS (1); approximately 4.6 cM proximal from SSR marker Bmac0113 in 5H bin 04 (1).

Description:

Plants are about 5/6 of normal height and awns are about 3/4 of normal length. The rachis internodes are slightly shorter than normal for Bowman. The seedling leaf of *brh7* plants is short and wide and leaf blades are wider than those of normal sibs. The Bowman line with *brh7* showed less lodging than Bowman. Although the kernels of *brh7* plants seem plumper and more globose shaped than those from normal sibs, the primary difference is a 10 to 15% reduction in kernel length. Kernel weights and grain yields of the *brh7* line are slightly lower than those of normal Bowman (1, 3).

Origin of mutant:

An induced mutant in Volla (PI 280423) (5).

Mutational events:

*brh7.w* (GSHO 1687, 7101, DWS1211) in Volla (PI 280423) (5, 6).

Mutant used for description and seed stocks:

*brh7.w* (GSHO 1687) in Volla; *brh7.w* in Bowman (PI 483237)\*7 (GSHO 1943, BW099, NGB 20505).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
6. Gaul, H. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:81.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:203.

J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:98.

BGS 42, Pyramidatum 1, *Pyr1*

Stock number: BGS 42  
Locus name: Pyramidatum 1  
Locus symbol: *Pyr1*

Previous nomenclature and gene symbolization:

Pyramidatum g = *Pyr.g* (5).

Pyramidatum i = *pyr.i* (5).

Inheritance:

Monofactorial recessive (2), which enhances the effects of *Zeo2* (Zeocriton 2) (2, 3). Located in chromosome 3HL (2); *Pyr1.g* is associated with SNP markers 2\_0410 to 1\_0926 (positions 61.77 to 85.26 cM) in 3H bin 05 of the Bowman backcross-derived line BW660 and with a marker in 2HL bin 13 where *Zeo2* (Zeocriton 2) locus is located; *Pyr1.i* (previously *Pyr2.i*) is associated with SNP markers 1\_0825 to 2\_0704 (positions 61.77 to 100.48 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW661 and with markers in 2HL bin 13 where *Zeo2* (Zeocriton 2) locus is located; *pyr1.aw* (previously *pyr.aw*) is associated with SNP markers 2\_0890 to 2\_0704 (positions 82.03 to 100.48 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW662 (2), in 3H bin 05.

Description:

Hayes and Harlan (6) reported that one gene controlled spike density in the line Pyramidatum. Spike shape, parallel vs. truncate pyramidal, is considered of limited value as a key character, but it is used in description of barley cultivars (1). Spikes are about 2/3 of normal length and have rachis internode length values of about 2.5 mm. Plants homozygous for *Pyr1.g* have pyramid-shaped spikes because lower rachis internodes shorter than upper ones. Spikes of heterozygous plants are parallel or strap-shaped. Plants homozygous for *Pyr1.a* are slightly shorter and have stiffer straw (3). When combined with *Zeo2* (Zeocriton 2), spikes of *Pyr1* plants are about 2/3 of normal length and have rachis internode length values of about 2.3 mm. The plants have pyramid-shaped spikes because lower rachis internodes are shorter than upper ones. The Bowman backcross-derived lines BW660 and BW661 have this phenotype. BW662, also derived from Pokko, has a similar 3H segment retained, but rachis internodes are only slightly shorter than those of Bowman, 3.6 vs. 4.5 mm (3). Unlike BW660 and BW661, BW662 does not have SNP marker 2\_0590 (position 218.47 cM) in 2H bin 13 (2). The semi-compact spike trait of BW662 was associated with a recessive inheritance pattern in backcross-derived progenies. Culms and peduncles of plants in lines BW660 and BW661 were 10 to 20% shorter than Bowman while a height reduction was not observed in BW662 (3). Kernel shapes and weights and grain yields of the BW lines for *Pyr1* were similar to those of Bowman (3).

Origin of mutant:

Probably natural occurrence in Finnish cultivars (3), but isolated from a backcross of Pokko (PI 467770) to Hja80001 (GSHO 1689, DWS1246), which is a gamma-ray induced, brachytic mutant from Aapo (PI 467771) (7).

Mutational events:

*Pyr1.g* in Hja64202 (Pokko\*3/Hja80001 mutant, DWS1242, GSHO 1581) (4, 7).

Mutant used for description and seed stocks:

*Pyr1.g* (GSHO 1581) in Hja64202; *Pyr1.g* in Bowman (PI 483237)\*7 (GSHO 2149, BW660, NGB 22225); *Pyr1.i* from Pokko mutant Hja79010 (Pokko\*3/Hja80001 mutant, GSHO 1582) (7) in Bowman\*6 (GSHO 1941), in Bowman\*7 (BW661, NGB 22226); *pyr1.aw* from Hja80089 (7) in Bowman\*7 (GSHO 2040, BW662, NGB 22227).



References:

1. Åberg, E., and G.A. Wiebe. 1946. Classification of barley varieties grown in the United States and Canada in 1945. U. S. Dept. Agr., Tech. Bull. 907. 190 pp., illus.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1999. Coordinator's report: Semidwarf genes. *Barley Genet. Newsl.* 29:74-79.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
6. Hayes, H.K., and H.V. Harlan. 1920. The inheritance of the length of internode in the rachis of the barley spike. U.S. Dept. Agr., Bull. 869. 26 pp.
7. Kivi, E.I. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:82.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:78-79.

BGS 43, Multiovary 1, *mov1*

Stock number: BGS 43  
Locus name: Multiovary 1  
Locus symbol: *mov1*

Previous nomenclature and gene symbolization:

Multiovary 5 = *mo5* (4).  
Multiovary 6 = *mo6b* (2, 3).

Inheritance:

Monofactorial recessive (2).  
Located in chromosome 7HL in bin 7H-07 (2, 3); near the *Amy2* (alpha-amylase 2) locus (2); co-segregation with molecular markers *Hsp17* and JS192.5 (3).

Description:

The *mov1.f* (*mov6b*) mutant has four carpels and two sepal-like structures where the lodicules should be. Stamens and lodicules are absent. It is presumed that the three stamens found in wild-type flowers have been converted into three additional carpels and that the lodicules have become leaf-like structures (3). The plant appears normal, but is completely sterile. The stock must be maintained as a heterozygote (1). This mutant appears morphologically similar to the *mo5* mutant (4), which was reported to map to the same region of chromosome 7HL (5). A seed stock was, however, not available for allelism tests (3).

Origin of mutant:

A fast neutron induced mutant in Steptoe (Clho 15229) (2).

Mutational events:

*mov1.f* (*mo6b*, FN 1) in Steptoe (Clho 15229) (1); *mov1.e* (*mo5*) (3, 4); *mov1.i* (5102, *mo6c*), *mov1.j* (5103, *mo6d*) from the Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany (3).

Mutant used for description and seed stocks:

*mov1.f* (FN 1) in Steptoe; *mov1.f* from Steptoe in Bowman (PI 483237)\*4 (BW523, NGB 22158).

References:

1. Kleinhofs, A. (Unpublished).
2. Soule, J., I. Skodova, D. Kudrna, A. Kilian, and A. Kleinhofs. 1995. Molecular and genetic characterization of barley flower development mutants. *Barley Genet. Newsl.* 25:76-80.
3. Soule, J.D., D.A. Kudrna, and A. Kleinhofs. 2000. Isolation, mapping, and characterization of two barley multiovary mutants. *J. Hered.* 91:483-487.
4. Tazhin, O.T. 1980. The linkage of the genes *mo5* and *n* in barley. *Barley Genet. Newsl.* 10:69-72.
5. Tazhin, O.T. 1982. Value of crossing-over between linked genes *mo5* and *n* in barley. *Barley Genet. Newsl.* 12:18-21.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:185.

BGS 44, Brachytic 16, *brh16*

Stock number: BGS 44  
Locus name: Brachytic 16  
Locus symbol: *brh16*

Previous nomenclature and gene symbolization:

Brachytic-v = *brh.v* (2).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 7HL (1); approximately 7.4 cM proximal from SSR marker

Bmag0135 in bin 7H bin 13 (1).

Description:

Plants are less than 2/3 of normal height and awns are about 3/4 of normal length in the Bowman backcross-derived line. The peduncle is about 2/3 normal length. The rachis internodes are slightly shorter than normal. The tip of the spike has a fasciated appearance because spikelets are very close together. The seed yield of the Bowman line with *brh16* was less than 1/3 of Bowman's yield. Since kernels per spikes and kernel size were not reduced, much of the yield loss was probably associated with reduced tillering (1). The original introduction (HE 2816) contained two dwarf mutants, but only *brh16.v* gene was isolated in the Bowman backcross-derived line.

Origin of mutant:

Probably an ethyl methanesulphonate induced mutant in Korál (PI 467778) (4).

Mutational events:

*brh16.v* in HE 2816 (DWS1176, GSHO 1686) from a cross between two semidwarf mutants (3, 4).

Mutant used for description and seed stocks:

*brh16.v* in HE 2816/Bowman (GSHO 1686); *brh16.v* in Bowman (PI 483237)\*7 (GSHO 2177, BW087, NGB 20494).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
4. Váša, M. 1986. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:204.

BGS 045, Semidwarf 4, *sdw4*

Stock number: BGS 045  
Locus name: Semidwarf 4  
Locus symbol: *sdw4*

Previous nomenclature and gene symbolization:

Culm length QTL on 7H = qCUL.ak-7H (4).

Inheritance:

Monofactorial recessive (3, 7).

Location in chromosome 7HL (4); about 1.2 cM from codominant STS marker ABG608 in bin 11 (3, 4); near DArT marker bPb-2328 in 7HL (6); *sdw4.ba* is associated with SNP markers 1\_1243 to 2\_1363 (positions 167.56 to 198.70 cM) in 7H bins 10 to 12 of the Bowman backcross-derived line BW831 (1); likely in 7H bin 11.

Description:

Semidwarf 4 (*sdw4*) is a monofactorial recessive that reduces culm length by about 20 to 30% (4, 6) by affecting the length of the 3<sup>rd</sup> and 4<sup>th</sup> culm internodes proportional more than the upper internodes (3, 4). The *sdw4* gene was associated with reduced lodging (4). Combining *sdw4* with *uzu1* (*uzu1*) reduced plant height further (3). In the Bowman backcross-derived line for *sdw4.ba* (BW831), plants were shorter, but the culms were slightly more robust and the flag leaves were larger than those of Bowman. Delayed heading was observed in plants with the *sdw4.ba* gene in some genetic backgrounds (2). The *sdw4.ba* mutation in China was reported to have originated as dwarf mutant (68-142) induced in the late 1960s by gamma-rays in the Chinese landrace Zhenongguangmangerleng (7). The first cultivar containing this mutant was Zhepi 1, released in 1978 by the Zhejiang Academy of Agricultural Science (7). Most cultivars now grown in the lower valley of Yangtze River were selected from crosses to Zhepi 1 (7).

Origin of mutant:

A gamma-ray induced mutant in the Chinese landrace Zhenongguangmangerleng (6); a spontaneous variant in the Japanese cultivar Kanto Nakate Gold (OUJ 518) released in 1953 (4), both parents of Kanto Nakate Gold, Shikoku (OUJ 546) and Golden Melon (OUJ808. PI 263410) are tall cultivars (4, 5).

Mutational events:

*sdw4.ba* (68-142) in Zhenongguangmangerleng (6), in the Japanese cultivar Kanto Nakate Gold (OUJ 518, PI383933) (4). Based on morphological traits and chromosomal location of mutant, both mutational events are very similar.

Mutant used for description and seed stocks:

*sdw4.ba* in Zhepi 1 and Zhenongda 7; *sdw4.ba* in Kanto Nakate Gold (OUJ 518; PI 383933), *sdw4.ba* from Zhenongda 7 in Bowman\*2 (BW831, NGB 22268).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Sameri, M., S. Nakamura, S.K. Nair, K. Takeda, and T. Komatsuda. 2009. A quantitative trait locus for reduced culm internode length in barley segregates as a Mendelian gene. *Theor. Appl. Genet.* 118:643-652.
4. Sameri, M., K. Takeda, and T. Komatsuda. 2006. Quantitative trait loci controlling agronomic traits in recombinant inbred lines from a cross of oriental- and occidental-type barley cultivars. *Breed. Sci.* 56:243-252.

5. Takahashi, R., S. Yasuda, J. Hayashi, T. Fukuyama, I. Moriya, and T. Konishi. 1983. Catalogue of barley germplasm preserved in Okayama University. Inst. Agr. Biol. Sci., Okayama Univ., Kurashiki, Japan. 217 p.
6. Yu, G.T., R.D. Horsley, B. Zhang, and J.D. Franckowiak. 2010. A new semi-dwarfing gene identified by molecular mapping of quantitative trait loci in barley. Theor. Appl. Genet. 120:853-861.
7. Zhang, J., and W. Zhang. 2003. Tracing sources of dwarfing genes in barley breeding in China. Euphytica 131:285-292.

Prepared:

J.D. Franckowiak and G.T. Yu. 2011. Barley Genet. Newsl. 41:80-81.

BGS 51, Rattail spike 1, *rtt1*

Stock number: BGS 51  
Locus name: Rattail spike 1  
Locus symbol: *rtt1*

Previous nomenclature and gene symbolization:

Rattail spike = *rt* (2).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 2HS (1); about 6.0 cM distal from the *fch15* (chlorina seedling 15) locus (1).

Description:

Spikes are highly modified with numerous immature spikelets and complete sterility. The arrangement of bracts in the spikelets suggests that they contain numerous florets.

Because the homozygous recessive is completely sterile, the stock must be maintained in the heterozygous condition (1). A semidominant interaction between *rtt1.a* and one version of the normal allele (*Rtt1.b* or *Rt'*) in Okaiku 3 is reported by Takahashi et al. (3).

Origin of mutant:

A spontaneous mutant in Goldfoil (PI 5975) (1).

Mutational events:

*rtt1.a* (GSHO 216) in Goldfoil (PI 5975); *Rtt1.b* (*Rt'*) in Okaiku 3 (OUL011) (3).

Mutant used for description and seed stocks:

*rtt1.a* (GSHO 216) in Goldfoil

References:

1. Robertson, D.W. 1967. Linkage studies of various barley mutations (*Hordeum* species). Crop Sci. 7:41-42.
2. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.
3. Takahashi, R., J. Hayashi, and I. Moriya. 1976. New find of an allele *Rt'* semi-dominant over *rt* for rattail spike. Barley Genet. Newsl. 6:74.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:111.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:87.

BGS 52, Chlorina seedling 15, *fch15*

Stock number: BGS 52  
Locus name: Chlorina seedling 15  
Locus symbol: *fch15*

Previous nomenclature and gene symbolization:

Orange seedling = *or* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HS (3); about 18.5 cM distal from the *fch1* (chlorina seedling 1) locus (2, 3); associated with SNP markers 2\_1338 to 2\_0699 (positions 74.97 to 126.33 cM) in 2H of the Bowman backcross-derived line BW357 (1), likely in 2H bin 06.

Description:

The normal color of seedlings is altered to "apricot yellow" when plants are grown in the field under low temperature. Plants respond better to higher temperatures and can be grown to maturity in suitable environments (3, 4). The yellow plant color is stable nearly to maturity (4).

Origin of mutant:

A spontaneous mutant in Trebi (PI 537442) (3).

Mutational events:

*fch15.x* (*or1.a*) (Trebi IV, GSHO 49) in Trebi (PI 537442) (3).

Mutant used for description and seed stocks:

*fch15.x* (GSHO 49) in Trebi, *fch15.x* in Bowman (PI 483237)\*2 (BW357, NGB20596).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology Epubl.* 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Robertson, D.W. 1967. Linkage studies of various barley mutations (*Hordeum* species). *Crop Sci.* 7:41-42.
3. Robertson, D.W., and O.H. Coleman. 1940. The addition of two factors for chlorophyll-deficient seedlings to the linkage groups of barley. *J. Genet.* 39:401-410.
4. Tsuchiya, T. 1971. Viability of *or* (orange seedling) homozygotes. *Barley Genet. Newsl.* 1:65-66.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:112.

Revised:

- T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:104.  
J.D. Franckowiak and A. Hang. 1997. *Barley Genet. Newsl.* 26:88.  
J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:48.

BGS 53, Albino seedling 2, *abo2*

Stock number: BGS 53  
Locus name: Albino seedling 2  
Locus symbol: *abo2*

Previous nomenclature and gene symbolization:

Albino 1 = *a1* (2).  
Albino seedling 2 = *a2* (4).

Inheritance:

Monofactorial recessive (1, 2).  
Located in chromosome 2HS (4); about 13.0 cM distal from the *fch1* (chlorina seedling 1) locus (4); about 5.5 cM proximal from the *fch15* (chlorina seedling 15) locus (4); over 9.4 cM distal from the *msg2* (male sterile genetic 2) locus (3).

Description:

Seedlings lack normal pigmentation; they are white and die at a two or three leaf stage (1, 2). Robertson's notes indicate that an albino 4 stock [*abo4* (*a4*)] may have been used in his linkage studies instead of the albino 2 stock [*abo2* (*a2*)] (4). The *abo2.b* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in an unknown cultivar (1).

Mutational events:

*abo2.b* (GSHO 70) in Nilsson-Ehle No 2 (3).

Mutant used for description and seed stocks:

*abo2.b* (GSHO 70) in Nilsson-Ehle No 2

References:

1. Hallqvist, C. 1926. Koppelungen und synthetische Lethalität bei den Chlorophyllfaktoren der Gerste. *Hereditas* 8:229-254.
2. Nilsson-Ehle, H. 1922. Über freie Kombination und Koppelung verschiedener Chlorophyllerbinheiten bei Gerste. *Hereditas* 3:191-199.
3. Rahman, M.M., and R.F. Eslick. 1975. Linkage of male sterile genes with seedling lethal genes. *Barley Genet. Newsl.* 5:42-44.
4. Robertson, D.W. 1967. Linkage studies of various barley mutations (*Hordeum* species). *Crop Sci.* 7:41-42.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:113.

Revised:

T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:105.  
A. Hang and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:89.



BGS 55, Chlorina seedling 1, *fch1*

Stock number: BGS 55  
Locus name: Chlorina seedling 1  
Locus symbol: *fch1*

Previous nomenclature and gene symbolization:

Chlorina seedling = *f* (6).  
Light green = *lg* (5).  
Light green 8 = *lg8* (4).  
Light green 10 = *lg10* (4).

Inheritance:

Monofactorial recessive (3, 5, 6).  
Located in chromosome 2HS (3, 10); in the centromeric region and about 4.0 cM distal from the *eog1* (elongated outer glume 1) locus (3, 7); associated with SNP markers 1\_1493 to 2\_0458 (positions 76.05 to 96.47 cM) in 2HS of the Bowman backcross-derived line BW351 (1), likely in 2H bin 07.

Description:

Seedling and immature leaves are very pale yellow-green (chlorophyll deficient) (6). The leaves gradually change to a green color beginning with the leaf tip. Plants can be grown to maturity in the field, but they have a slightly yellow-green color and are stunted easily by stress. Plants of the Bowman backcross-derived line BW351 headed about 10 days later than Bowman and were slightly shorter. Plants produced a few more kernels per spike and rachis internodes were slightly shorter. Kernels were 10 to 15% lighter and they were slightly shorter and thinner. Grain yields were 1/2 to 2/3 of normal (2).

Origin of mutant:

A spontaneous mutant in Golden (Gull, CIho 1145, GSHO 466) (6).

Mutational events:

*fch1.a* (GSHO 112) in Gull (CIho 1145, GSHO 466) (6, 9); *fch1.p* (*lg*) (Minn 80, GSHO 548) (5, 9); *fch1.q* (*lg8*) (No 155, GSHO 8) (4, 8); and *fch1.r* (*lg10*) (No 157, GSHO 154) in Himalaya (CIho 1312) (4).

Mutant used for description and seed stocks:

*fch1.p* (GSHO 548) in Minn 84-7; *fch1.p* in Bowman (PI 483237)\*9 (GSHO 1886, BW351, NGB 20690).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Hallqvist, C. 1926. Koppelungen und synthetische Lethalität bei den Chlorophyllfaktoren der Gerste. *Hereditas* 8:229-254.
4. Haus, T.E. 1973. Allelism among light green, *lg*, seedling mutants. *Barley Genet. Newsl.* 3:17-18.
5. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. *Genetics* 28:419-420.
6. Nilsson-Ehle, H. 1922. Über freie Kombination und Koppelung verschiedener Chlorophyllerbinheiten bei Gerste. *Hereditas* 3:191-199.
7. Robertson, D.W., G.W. Deming, and D. Koonce. 1932. Inheritance in barley. *J. Agric. Res.* 44:445-466.
8. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies

in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.

9. Tsuchiya, T. 1974. Allelism of *f* for chlorina and *lg* for light green (chlorina) in chromosome 2S in barley. Barley Genet. Newsl. 4:79.

10. Tsuchiya, T., and R.J. Singh. 1973. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 3:75-79.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:115.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:106.

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:90.

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:49-50.

BGS 56, White streak 4, *wst4*

Stock number: BGS 56  
Locus name: White streak 4  
Locus symbol: *wst4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HL (1, 2, 3); about 6.5 cM distal from the *eog1* (elongated outer glume 1) locus (2).

Description:

Mutants grown at low temperatures exhibit numerous, wide, chlorotic (white) streaks on developing leaves. If temperatures are continuously low, plants appear highly chlorotic. As temperature rises, the white streaks gradually disappear. Exposure to 3EC for two weeks after sowing is sufficient to induce distinct streaks in the first and second leaves (2).

Origin of mutant:

A spontaneous mutant in Kanyo 7 (OUK651) (2).

Mutational events:

*wst4.d* (OUL068) in Kanyo 7 (2).

Mutant used for description and seed stocks:

*wst4.d* (GSHO 568) in Kanyo 7; *wst4.d* in Bowman (PI 483237)\*4 (GSHO 1905); *wst4.d* in Bowman\*7 (BW913, NGB 22344).

References:

1. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 4:66-69.
2. Takahashi, R., and I. Moriya. 1969. Inheritance and linkage studies in barley. IV. Linkages of four variegated mutants. Ber. Ohara Inst. landw. Biol., Okayama Univ. 15:35-46.
3. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. Barley Genet. Newsl. 2:93-98.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl.1:116.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:91.

BGS 57, Elongated outer glume 1, *eog1*

Stock number: BGS 57  
Locus name: Elongated outer glume 1  
Locus symbol: *eog1*

Previous nomenclature and gene symbolization:

Extended outer glumes = *e* (7).  
Wide glumes = *w* (7).  
Macrolepis = *lep-e* (*lep-a*) (5, 10, 11).  
Long outer glume = *log* (12).  
Elongated outer glume = *e* (3, 12).

Inheritance:

Monofactorial recessive (1, 2, 13).  
Located in chromosome 2HL (4); about 30.5 cM proximal from the *vrs1* (six-rowed spike 1) locus (3, 8).

Description:

A multiple allelic series exists at this locus, which controls increased size of the outer glumes (glumes) of the spikelet. Glume width varies from 2.5 to 4.0 mm depending on genetic background and specific allele (13, 14). Glume awn length varies from awnless to nearly as long as the lemma awn (92 mm) depending on the *eog1* allele present and genes at other loci (7, 13), but some confusion has occurred regarding alleles at the *eog1* locus and expression of other glume characteristics (12, 13). The size of the glume may range from less than twice normal width in Clho 14955 to lemma-like glumes in Triple Bearded Mariout.

Origin of mutant:

A spontaneous mutant and natural occurrence in a few cultivars (1, 13).

Mutational events:

*eog1.a* in Triple Bearded Mariout (Clho 2523, GSHO 29) (4, 13); *lep-e.1* (NGB 114210, GSHO 960), -*e.2* (NGB 114211) in Gull (Clho 1145), -*e.3* (NGB 114212), -*e.4* (NGB 114213), -*e.5* (NGB 114214), -*e.6* (NGB 114215), -*e.7* (NGB 114216), -*e.8* (NGB 114217), -*e.9* (NGB 114218), -*e.10* (NGB 114219), -*e.11* (NGB 114220), -*e.12* (NGB 114221), -*e.13* (NGB 114222), -*e.29* (NGB 114239), -*e.34* (NGB 114244), -*e.42* (NGB 114253, NGB 114386), -*e.45* (NGB 114258), -*e.49* (NGB 114265), -*e.50* (NGB 114266), -*e.51* (NGB 114267), -*e.52* (NGB 114268), -*e.53* (NGB 114269), -*e.54* (NGB 114270) in Bonus (PI 189763), -*e.14* (NGB 114223), -*e.15* (NGB 114224), -*e.16* (NGB 114225), -*e.17* (NGB 114226), -*e.18* (NGB 114227), -*e.19* (NGB 114228, NGB 114229), -*e.20* (NGB 114230), -*e.21* (NGB 114231), -*e.22* (NGB 114232), -*e.23* (NGB 114233), -*e.24* (NGB 114234), -*e.25* (NGB 114235), -*e.26* (NGB 114236), -*e.27* (NGB 114237), -*e.28* (NGB 114238), -*e.30* (NGB 114240), -*e.31* (NGB 114241), -*e.32* (NGB 114242), -*e.33* (NGB 114243), -*e.38* (NGB 114248) in Foma (Clho 11333), -*e.35* (NGB 114245), -*e.36* (NGB 114246), -*e.37* (NGB 114247), -*e.39* (NGB 114249, NGB 114250), -*e.40* (NGB 114251), -*e.41* (NGB 114252), -*e.43* (NGB 114254, NGB 114255), -*e.44* (NGB 114256), -*e.46* (NGB 114257), -*e.47* (NGB 114261, NGB 114262), -*e.48* (NGB 114263, NGB 114264) in Kristina (NGB 1500) (5, 9, 10, 11); *eog1.b* in PI 173567 (G 8) (14); *eog1.c* in Clho 14955; *eog1.d* (Mut 3447/64) in Proctor (PI 280420) (6).

Mutant used for description and seed stocks:

*eog1.a* in Triple Bearded Mariout (Clho 2523, GSHO 29); *lep-e.1* (GSHO 960, NGB 114210) in Gull (Clho 1145); *eog1.a* in Bowman (PI 483237)\*7 (GSHO 1891, BW299, NGB 20583); *eog1.c* from Clho 14955 in Bowman\*7 (GSHO 1892, BW300, NGB 20584).

References:

1. Biffen, R.H. 1906. Experiments on the hybridisation of barleys. Proc. Cambridge Phil. Soc. 13:304-308.
2. Biffen, R.H. 1907. Studies in the inheritance of disease-resistance. J. Agric. Sci. 2:109-128.
3. Bose, R.D., M.A. Aziz, and M.P. Bhatnagar. 1937. Studies in Indian barleys. IV. The inheritance of some anatomical characters responsible for lodging and of some ear-head characters in an interspecific cross between two Pusa barleys. Indian J. Agric. Sci. 7:48-88.
4. Griffiee, F. 1925. Correlated inheritance of botanical characters in barley, and the manner of reaction to *Helminthosporium sativum*. J. Agric. Res. 30:915-925.
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
6. Häuser, H., and G. Fischbeck. 1972. Translocations and genetic analysis of other mutants. Barley Genet. Newsl. 2:28-29.
7. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
8. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.
9. Lundqvist, U. 1994. Coordinator's report: Ear morphology genes. Barley Genet. Newsl. 23:175-176.
10. Nötzel, H. 1952. Genetische Untersuchungen an röntgeninduzierten Gerstenmutanten. Kühn-Archiv. 66:72-132.
11. Nybom, N. 1954. Mutation types in barley. Acta Agric. Scand. 4:430-456.
12. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1955. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement II, 1947-1953. Agron. J. 47:418-425.
13. Tsuchiya, T. 1974. Preliminary results on genetic studies of outer glume characters in barley. Barley Genet. Newsl. 4:76-78.
14. Tsuchiya, T. 1974. Further results of allelism testing in barley. Barley Genet. Newsl. 4:82-85.

Prepared:

T. Tsuchiya. 1975. Barley Genet. Newsl. 5:101.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:92-93.4

BGS 58, Six-rowed spike 1, *vrs1.c*

Stock number: BGS 58  
Locus name: Six-rowed spike 1  
Locus symbol: *vrs1.c* = *lr*

Previous nomenclature and gene symbolization:

Reduced lateral spikelet appendage on the lemma = *lr* (3).

Reduced lateral spikelet appendage on the lemma = *v<sup>lr</sup>* (5).

Inheritance:

An incomplete dominant in the multiple allelic series at the *vrs1* (six-rowed spike 1) locus (1, 3, 5).

Located in chromosome 2HL (3); about 15.4 cM distal from the *Gth1* (toothed lemma 1) locus (6); 26.5 cM distal from the *eog1* (elongated outer glume 1) locus (2).

Description:

The spike has long awns on the lemma of the central spikelet and awn-like appendages on the lemma of the lateral spikelets (1, 5). Lateral spikelets have perfect flowers and complete fertility. The *lr* trait is expressed only in six-rowed barley, and heterozygotes have a short awn on the lemma of lateral spikelets (3, 5). Since recombination with neither *vrs1.a* (*v*) nor *Vrs1.b* (*V*) alleles was observed (3, 5), the *lr* or *vrs1.c* phenotype is likely controlled by an allele at the *vrs1* locus (5). The Bowman backcross-derived line for the *vrs1.c* gene has short, stiff awns on the central spikelets (about 1/3 normal length) and no awns on the lateral spikelets.

Origin of mutant:

Natural occurrence in Nudihaxtoni (PI 32368) (1) and Bozu types of barley (4, 5).

Mutational events:

*vrs1.c* (*lr*) (GSHO 153) in *Hordeum intermedium* var Nudihaxtoni (1).

Mutant used for description and seed stocks:

*vrs1.c* (*lr*) (GSHO 153) in *Hordeum intermedium* var Nudihaxtoni; *vrs1.c* in Bowman (PI 483237)\*7 (GSHO 1908, BW899, NGB 22331).

References:

1. Glinyany, N.P. 1937. Inheritance of awns and furcas (hoods) in crosses between *Hordeum vulgare* var. *Nudihaxtoni* X *Hordeum vulgare* var. *Trifurcatum*. Bull. Appl. Bot., Genet. & Pl. Breed. II. 7:355-376. [In Russian with English summary.].
2. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.
3. Leonard, W.H. 1942. Inheritance of reduced lateral spikelet appendages in the Nudihaxtoni variety of barley. J. Am. Soc. Agron. 34:211-221.
4. Takahashi, R., and J. Hayashi. 1982. Studies on classification and inheritance of barley varieties having awnless or short-awned lateral spikelets (Bozu barley). II. Mode of inheritance and spike characteristics of Bozu barley. Nogaku Kenyu 60:25-37. [In Japanese with English summary.].
5. Takahashi, R., J. Hayashi, I. Moriya, and S. Yasuda. 1982. Studies on classification and inheritance of barley varieties having awnless or short-awned lateral spikelets (Bozu barley). I. Variation of awn types and classification. Nogaku Kenyu 60:13-24. [In Japanese with English summary.].
6. Wexelsen, H. 1934. Quantitative inheritance and linkage in barley. Hereditas 18:307-308.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:118.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:94.

BGS 59, Grandpa 1, *gpa1*

Stock number: BGS 59  
Locus name: Grandpa 1  
Locus symbol: *gpa1*

Previous nomenclature and gene symbolization:

Grandpa = *gp* (1).  
Grandpa 2 = *gp2* (5, 6).

Inheritance:

Monofactorial recessive (1).  
Located in chromosome 2HL (4, 5); about 24.5 cM distal from the *lig1* (liguleless 1) locus (3).

Description:

Seedlings display a pattern of transverse of alternating white and green bands on the first, second, and occasionally the third foliage leaves. Plants have a slightly pale green color prior to heading. Grandpa plants are sensitive to flooding and produce an albino flag leaf, peduncle, and spike (3). Plants are viable in the field, but the seed is thin and yields are low (4).

Origin of mutant:

A spontaneous mutant in Lyallpur (NSL 40271) isolated by GA Wiebe (2).

Mutational events:

*gpa1.a* (CIho 6854, GSHO 519) in Lyallpur (NSL 40271) (2); *gpa1.b* (*gp2*) (GSHO 1379) in Montcalm (CIho 7149) (3, 5, 6).

Mutant used for description and seed stocks:

*gpa1.b* (GSHO 1379) in Montcalm; *gpa1.b* in Bowman (PI 483237)\*7 (GSHO 1934, BW397, NGB 22147).

References:

1. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. *Genetics* 28:419-440.
2. Martini, M.L., and H. V. Harlan. 1942. Barley freaks. *J. Hered.* 33:339-343.
3. Matchett, R.W., H.G. Nass, and D.W. Robertson. 1971. Inheritance and linkage studies with the grandpa gene in barley, *Hordeum vulgare* L. *Can. J. Genet. Cytol.* 13:489-498.
4. Matchett, R.W., B.M. Pollock, and D.W. Robertson. 1968. The "grandpa" gene: A chlorophyll mutation in *Hordeum* species. *J. Hered.* 59:279-282.
5. Tsuchiya, T. 1971. Trisomic analysis of grandpa 2 (*gp2*). *Barley Genet. Newsl.* 1:62.
6. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. *Can. J. Genet. Cytol.* 5:200-219.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:119.

Revised:

T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:107.  
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:95.



BGS 60, Liguleless 1, *lig1*

Stock number: BGS 60  
Locus name: Liguleless 1  
Locus symbol: *lig1*

Previous nomenclature and gene symbolization:

Ligule and auricle less = *al* (9).

Liguleless = *li* (8).

Exauriculum = *aur-a* (1).

Inheritance:

Monofactorial recessive (9).

Located in chromosome 2HL (6, 9, 10); about 25.1 cM distal from the *mtt4* (mottled leaf 4) locus (2); and near AFLP marker E3633-1 in subgroup 21 of the Proctor/Nudinka map (7); associated with SNP markers 1\_0383 to 2\_0994 (positions 207.22 to 233.44 cM) in 2H bins 13 to 14 of the Bowman backcross-derived line BW483, and with SNP markers 1\_0446 to 2\_0994 (positions 199.54 to 233.44 cM) in 2H bins 12 to 14 of the Bowman backcross-derived line BW482 (1), likely in 2H bin 13.

Description:

The ligule and auricle of all leaves are absent, and the leaf blades are erect along the stem. Liguleless plants can be identified visually at all stages of growth (9). Reverse mutation of some mutants is possible (4). The fine structure analysis of the *lig1* locus conducted by Konishi (5) showed that some mutants can recombine. The Bowman backcross-derived lines with the *lig1* gene, BW482 and 483, are similar in maturity, agronomic traits, and yield to Bowman (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar, Muyoji (liguleless) (OUL007) (8).

Mutational events:

*lig1.my* as Muyoji (OUL007, GSHO 6) (9); *lig1.ky* in Koyo (PI 190819), *lig1.a1* (OUM001), *lig1.a2* in Akashinriki (PI 467400, OUJ659); *lig1.c1*, *lig1.c2*, *lig1.c3*, *lig1.c4* in Chikurin Ibaraki 1 (OUJ030, Clho 7370) (5); *aur-a.1* (*lig1.b1*) (NGB 114359), *aur-a.2* (*lig1.b2*) (NGB 114360), *aur-a.7* (*lig1.b7*) (NGB 114365), *aur-a.8* (*lig1.b8*) (NGB 114366), *aur-a.9* (*lig1.b9*) (NGB 114367) in Bonus (PI 189763), *aur-a.3* (*lig1.b3*) (NGB 114361), *aur-a.4* (*lig1.b4*) (NGB 114362), *aur-a.5* (*lig1.b5*) (NGB 114363), *aur-a.6* (*lig1.b6*) (NGB 114364), *aur-a.10* (*lig1.b10*) (NGB 114368) in Foma (Clho 11333) (5); *aur-a.11* (NGB 114369), *aur-a.12* (NGB 114370, NGB 114371) in Kristina, *aur-a.13* (NGB 114372), *aur-a.14* (NGB 114373) in Bonus, *aur-a.15* (NGB 119377) in Golf (PI 488529) (6); *lig1.2* in Bonus from the stock *eli-2* (eligulum-2) (NGB 115389) as the second mutant (1, 2).

Mutant used for description and seed stocks:

*lig1.my* (GSHO 6) as Muyoji; *lig1.my* in Bowman (PI 483237)\*8 (GSHO 1930, BW483, NGB 20711); *lig1.2* from a Bonus mutant (NGB 115389) in Bowman\*5 (BW482, NGB 20710).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
4. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VI. Ten mutant genes located on chromosomes 1 to 7, except 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:227-250.

5. Konishi, T. 1975. Reverse mutation at the ligule-less locus (*li*) of barley. BGN 5:21-23.
6. Konishi, T. 1981. Reverse mutation and interallelic recombination at the ligule-less locus in barley. p. 838-845. *In* M.J.C. Ascher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse. (eds.) Barley Genetics. IV. Proc. Fourth Int. Barley Genet. Symp. Edinburgh. Edinburgh University Press.
7. Lundqvist, U. (Unpublished).
8. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
9. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1955. A summary of linkage studies in barley: Supplement II, 1947-1953. Agron. J. 47:418-425.
10. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.
11. Woodward, R.W. 1957. Linkages in barley. Agron. J. 49:28-32.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:120.

Revised:

J.D. Franckowiak, U. Lundqvist, T. Konishi. 1997. Barley Genet. Newsl. 26:96.

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:205-206.

U. Lundqvist and J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:116-117.

BGS 61, Triple awned lemma 1, *trp1*

Stock number: BGS 61  
Locus name: Triple awned lemma 1  
Locus symbol: *trp1*

Previous nomenclature and gene symbolization:

Triple-bearded variation (5).  
Triple awned lemma = *tr* (4).

Inheritance:

Monofactorial recessive (4).  
Located in chromosome 4HL (2); *trp1.a* is associated with SNP markers 2\_1397 to 1\_0467 (positions 47.8 to 105.27 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW881 (2), likely in 4H bin 07. Previously located in chromosome 2HL (4, 7), over 35.5 cM distal from the *wst7* (white streak 7) locus (1), but the *wst7* locus is in a subterminal position in 2HL (2); near AFLP marker E3644-13 in subgroups 22 and 23 of the Proctor/Nudinka map (6).

Description:

Mutants may have three awns on the lemma instead of one, but expression is variable (5). The awn or hood extending from the lemma of the central spikelet forks to form one normal central appendage and one or two shorter lateral ones (4). Expression of triple awn trait in the Bowman backcross-derived line BW881 is reduced to an occasional branch in the basal part of the awn. However, when plants are grown under heat stress a stronger expression of the *trp1* trait was observed. Other morphological deviations from Bowman were not observed (3). The conflict in chromosome map positions suggests that strong expression of the triple awn phenotype may involve two loci (3).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (5), possibly of natural occurrence in six-rowed cultivars originating from East Asia (3).

Mutational events:

*trp1.a* in Triple-awn Lemma (CIho 6630, GSHO 210) (5).

Mutant used for description and seed stocks:

*trp1.a* in CIho 6630 (GSHO 210); *trp1.a* from CIho 6880 (Ahang/Twisted Flag//Triple-awn Lemma) in Bowman (PI 483237)\*7 (GSHO 1936, BW881, NGB 22315).

References:

1. Doney, D.L. 1961. An inheritance and linkage study of barley with special emphasis on purple pigmentation of the auricle. M.S. Thesis. Utah State Univ., Logan.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. *Genetics* 28:419-440.
5. Martini, M.L., and H.V. Harlan. 1942. Barley freaks. *J. Hered.* 33:338-343.
6. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.
7. Tsuchiya, T., and R.J. Singh. 1973. Further information on telotrisomic analysis in barley. *Barley Genet. Newsl.* 3:75-79.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:121.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:97.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:82-83.

BGS 62, Subjacent hood 1, *sbk1*

Stock number: BGS 62  
Locus name: Subjacent hood 1  
Locus symbol: *sbk*

Previous nomenclature and gene symbolization:

Subjacent hood = *sk* (9).  
Hooded awn 2 = *k2* (12).  
Hoods = *k<sub>r</sub>* (11).  
Calcaroides-a = *cal-a* (4, 5).

Inheritance:

Monofactorial recessive (8, 9).  
Located in chromosome 2HS (8, 9, 10); distal from molecular marker CDO057 (7); associated with SNP markers 1\_0326 and 1\_1059 (positions 16.91 and 17.96 cM) in 2HS of the Bowman backcross-derived line BW767, markers 1\_1059 to 2\_0563 (positions 17.96 to 21.19 cM) in 2HS of the Bowman backcross-derived line BW766, and marker 1\_0326 (2), in 2H bin 02.

Description:

Unlike the *Kap1* (hooded awn 1) mutants, the lemma appendage or its modification is situated somewhat below the top of the lemma. Lemma modifications may include a central cup-like cavity or sac in some alleles and/or pronounced lemma wings in other alleles (1, 7). The modified lemma bears a short distal awn. Only a few florets of the spike have malformations in alleles *cal-a.3*, *-a.6*, *-a.7*, and *-a.17* and these alleles are associated with the formation of pronounced wings (7). There are no rudiments of a floral organ within the hood-like cavity (7, 8, 9). Leaf knots and leaf curling are present in some alleles (7). In the homozygous condition, the *sbk1.a* gene is epistatic to *Kap1.a* and to *Lks1.a* (awnless) genes (8). Plants of the Bowman backcross-derived lines BW103, BW766, and BW767 were much less vigorous than Bowman, about 3/4 of normal height and 3 to 4 fewer fertile rachis nodes. The kernel of the BW766 and BW767 plants were about 1/2 of normal weight and grain yields were about 1/10 of normal. Plants of the BW103 line were more vigorous with kernel weights about 3/4 of those for Bowman and grain yield of about 1/2 of normal. The effects of the *sbk1* mutants on plant vigor were less pronounced in cooler environments (3).

Origin of mutant:

A spontaneous mutant identified as Tayeh 13 (OUC335) (6); an X-ray induced mutant in Bonus (PI 189763) (6).

Mutational events:

*sbk1.a* (GSHO 267) in Tayeh 13 (OUC335) (8); *cal-a.1* (NGB 114280, 114281) in Bonus (PI 189763) (5, 6); *cal-a.3* (NGB 114283), *-a.5* (NGB 114285) in Foma (CIho 11333); *cal-a.6* (NGB 114286) in Bonus; *cal-a.7* (NGB 114287), *-a.8* (NGB 114288, 114289), *-a.11* (NGB 114290, 114291), *-a.12* (NGB 114292), *-a.13* (NGB 114293) in Foma; *cal-a.16* (NGB 114295), *-a.17* (NGB 114296), *-a.20* (NGB 114299), *-a.21* (NGB 114300) in Bonus (5, 6); *sbk1.b* (*k<sub>r</sub>*) in Montcalm (CIho 7149) (11).

Mutant used for description and seed stocks:

*sbk1.a* (GSHO 267) in Tayeh 13; *sbk1.a* via R.I. Wolfe's Multiple Recessive Stock for chromosome 2 in Bowman (PI 483237)\*4 (BW766, NGB 22234); *sbk1.b* in Montcalm; *sbk1.b* from Montcalm in Bowman\*7 (GSHO 1874, BW767, NGB 22235); *cal-a.1* in Bonus (GSHO 286, NGB 114280, NGB 114281); *cal-a.1* from Bonus in Bowman\*3 (GSHO 2186); *cal-a.1* in Bowman\*6 (BW103, NGB 20509).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. In L. Munck, K. Kirkegaard, and B. Jensen (eds.).

- Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
  3. Franckowiak, J.D. (Unpublished).
  4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
  5. Lundqvist, U. 1993. Coordinator's report: Ear morphology genes. *Barley Genet. Newsl.* 22:137-139.
  6. Lundqvist, U. (Unpublished).
  7. Pozzi, C., P. Faccioli, V. Terzi, A.M. Stanca, S. Cerioli, P. Castiglioni, R. Fink, R. Capone, K.J. Müller, G. Bossinger, W. Rohde, and F. Salamini. 2000. Genetics of mutations affecting the development of a barley floral bract. *Genetics* 154:1335-1346.
  8. Takahashi, R., and J. Hayashi. 1966. Inheritance and linkage studies in barley. II. Assignment of several new mutant genes to their respective linkage groups by the trisomic method of analysis. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 13:185-198.
  9. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. *Ber. Ohara Inst. landw. Forsch.* 10:29-52.
  10. Tsuchiya, T., and R.J. Singh. 1973. Further information on telotrisomic analysis in barley. *Barley Genet. Newsl.* 3:75-79.
  11. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. *Can. J. Genet. Cytol.* 5:200-219.
  12. Woodward, R.W. 1957. Linkages in barley. *Agron. J.* 49:92-94.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:122.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:98.  
J.D. Franckowiak and U. Lundqvist. 2002. *Barley Genet. Newsl.* 32:83-84.  
J.D. Franckowiak and U. Lundqvist. 2010. *Barley Genet. Newsl.* 40:51-52.

BGS 63, Virescent seedling 1, *yvs1*

Stock number: BGS 63  
Locus name: Virescent seedling 1  
Locus symbol: *yvs1*

Previous nomenclature and gene symbolization:

Yellow seedling 1 =  $y$  (1, 3).  
Xantha (yellow) seedling  $x = y^x$  (5).  
Yellow seedling  $x = y_x$  (4).  
Albina seedling-c = *alb-c* (9).

Inheritance:

Monofactorial recessive (1, 6, 7).  
Located in chromosome 2HS (5); over 13.7 cM proximal from the *fch15* (chlorina seedling 15) locus (2, 6); about 2.0 cM proximal from the *fch1* (chlorina seedling 1) locus (2, 6).

Description:

Virescent seedlings have a slightly green tip, but fail to survive beyond the seedling stage (5, 7). Recessive alleles at the *yvs1* locus must be maintained as heterozygous stocks.

Origin of mutant:

A spontaneous mutant in a Swedish cultivar (1, 7).

Mutational events:

*yvs1.a* (GSHO 68) in a Swedish cultivar (1, 6); *yvs1.b* ( $y_x$ ) (GSHO 62) in Faust I (Clho 4579) (5); *alb-c.7* (NGB 14684) in Gull (Clho 1145) (8, 9, 10).

Mutant used for description and seed stocks:

*yvs1.a* (GSHO 68) in Minn 72-8.

References:

1. Hallqvist, C. 1924. Chlorophyllmutanten bei Gerste. Ihre Entstehung und primären Spaltungen. *Hereditas* 5:49-83.
2. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. *Genetics* 28:419-440.
3. Nilsson-Ehle, H. 1922. Über freie Kombination und Koppelung verschiedener Chlorophyllerbinheiten bei Gerste. *Hereditas* 3:191-199.
4. Robertson, D.W. 1971. Recent information of linkage and chromosome mapping. p. 200-242. In R.A. Nilan (ed.) *Barley Genetics II. Proc. Second Int. Barley Genet. Symp.*, Pullman, WA, 1969. Washington State Univ. Press, Pullman.
5. Robertson, D.W., and O. H. Coleman. 1940. The addition of two factors for chlorophyll-deficient seedlings to the linkage groups of barley. *J. Genet.* 39:401-410.
6. Robertson, D.W., and O. H. Coleman. 1942. Location of glossy and yellow seedlings in two linkage groups. *J. Am. Soc. Agron.* 34:1028-1034.
7. Robertson, D.W., G.W. Deming, and D. Koonce. 1932. Inheritance in barley. *J. Agric. Res.* 44:445-466.
8. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at the Carlsberg Laboratory. *Barley Genet. Newsl.* 21:102-108.
9. Wettstein, D. von, and K. Kristiansen. 1973. Stock list for nuclear gene mutants affecting the chloroplast. *Barley Genet. Newsl.* 3:113-117.
10. Wettstein, D. von, and K. Kristiansen. 1982. Chloroplast gene: Progress report II on diallelic tests between mapped chloroplast genes and chloroplast genes in stock collection at Copenhagen. *Barley Genet. Newsl.* 12:93-94.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:114 as BGS 54, Yellow seedling,  $y_x$ .

T. Tsuchiya and T.E. Haus. 1972. Barley Genet. Newsl. 2:180.

Revised:

A. Hang and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:99.



BGS 64, Desynapsis 7, *des7*

Stock number: BGS 64  
Locus name: Desynapsis 7  
Locus symbol: *des7*

Previous nomenclature and gene symbolization:  
None.

Inheritance:  
Monofactorial recessive (3).  
Located in chromosome 2H (1).

Description:  
The chromosomes are paired during the pachytene stage of microsporogenesis, but they undergo desynapsis during diplotene. The degree of desynapsis is  $d = 6.1 \pm 2.6$ , ranging from 7 ring bivalents ( $d = 0$ ) to 14 univalents ( $d = 14$ ). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 3.0 micronuclei per tetrad with a range of 0 to 13. Female fertility is about 33%, and about 13% of the selfed seeds are trisomics (1).

Origin of mutant:  
A spontaneous mutant in Betzes (PI 129430) (2, 3).

Mutational events:  
*des7.j* (GSHO 598) in Betzes (PI 129430) (3).

Mutant used for description and seed stocks:  
*des7.j* (GSHO 598) in Betzes.

References:  
1. Hernandez-Soriano, J.M. 1973. Desynaptic mutants in Betzes barley. M.S. Thesis. Univ. of Arizona, Tucson.  
2. Ramage, R.T., and J.M. Hernandez-Soriano. 1971. Desynaptic genes in Betzes barley. Barley Genet. Newsl. 1:38.  
3. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. Barley Genet. Newsl. 2:65-68.

Prepared:  
J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:130.

Revised:  
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:100.

BGS 65, Early maturity 1, *Eam1*

Stock number: BGS 65  
Locus name: Early maturity 1  
Locus symbol: *Eam1*

Previous nomenclature and gene symbolization:

Early maturity = *Ea* (3).  
Photoperiod response 1 = *Ppd-H1* (5).  
Early maturity 1 = *Ea1* (2).

Inheritance:

Monofactorial dominant (3, 7).  
Located in chromosome 2HS (1, 3, 6, 7); about 23.1 cM distal from the *com2* (compositum 2) locus (6).

Description:

This gene controls the strong response of some cultivars to photoperiod. The *Eam1* gene is described as a simply inherited dominant and the main factor for early maturity (1, 2, 3, 8). Under long-day condition, a near-isogenic line with *Eam1* is reported to be 7 to 8 days earlier than the *eam1* line 'ea1' (9). The early maturity gene is weakly linked to the *vrs1* (six-rowed spike 1) locus (1, 8, 10). In North Dakota, USA, progenies from crosses of Bowman to *Hordeum vulgare* subsp. *spontaneum* and Coast, facultative winter, northern spring (from Finland and Alaska), and winter types of barley, extremely early segregates are found. A linkage between early maturity and malformed spikes (*com2*) is observed when an accession from the ICARDA-CIMMYT collection of barley freaks is backcrossed to Bowman. Positive linkage data are found also in progenies from some crosses between a line having the *com2* - *eam1* recombinant and early segregates from the above crosses (2, 6). The *Eam1* locus in barley is likely homoeologous to the *Ppd1*, *Ppd2*, and *Ppd3* loci in wheat, which control strong photoperiod response (5).

Origin of mutant:

The strong photoperiod response to short nights occurs naturally in many barley cultivars and its wild relative, *Hordeum vulgare* subsp. *spontaneum*.

Mutational events:

A single dominant gene controls early maturity based on a cross to Lion (*Eam1.b*) (PI 32767, GSHO 27) (3); *Eam1.e* (GSHO 1569) isolated as Prior (PI 221325) as a mutant or outcross (4, 9); *eam1.a* is the normal allele in Manchurian six-rowed cultivars (2, 9); *eam1.a* is the allele present likely in most two-rowed cultivars from Europe (9).

Mutant used for description and seed stocks:

*Eam1.c* in Estate (PI 57700, GSHO 1316); *Eam1.c* from Estate in Bowman (PI 483237)\*7 (GSHO 1871); *Eam1.c* in Bowman\*8 (BW280, NGB 20564); *Eam1.d* from KT1031 (a winter barley from Bulgaria, GSHO 1568) in Bowman\*9 (GSHO 1872, BW281, NGB 20564); *Eam1.e* from Prior in Betzes\*7 (Erbet, CIho 13826) (4).

References:

1. Barbacki, S. 1930. [Studies in barley. II. Variability and inheritance of some physiological characters. The importance of breeding characters]. Men. Inst. Nat. Polon. Ec. Rur. Puawy 11:579-610. [In Polish with English summary.]
2. Franckowiak, J.D. 1992. Mapping a gene for photoperiod sensitivity in barley. Agron. Abstr. 1992:96.
3. Griffee, F. 1925. Correlated inheritance of botanical characters in barley, and the manner of reaction to *Helminthosporium sativum*. J. Agric. Res. 30:915-935.
4. Hockett, E.A., and R.F. Eslick. 1972. Registration of Erbet barley (reg. no. 127). Crop

Sci. 12:712-713.

5. Laurie, D.A., N. Pratchett, J.H. Bezant, and J.W. Snape. 1994. Genetic analysis of a photoperiod response gene on the short arm of chromosome 2 (2H) of *Hordeum vulgare* (barley). *Heredity* 72:619-627.

6. Luna Villafañá, A. 1995. Mapping marker genes in chromosome 2 of barley. M.S. Thesis. North Dakota State Univ., Fargo.

7. Mackie, W.W. 1926. Inheritance of resistance to *Helminthosporium californium* in a cross between Chevalier barley, a resistant variety, and Abyssinian, a susceptible variety. *Phytopathology* 16:764. [Abstr.]

8. Neatby, K.W. 1929. An analysis of the inheritance of quantitative characters and linkage in barley. *Sci. Agric.* 9:701-718.

9. Smail, V.W., R.F. Eslick, and E.A. Hockett. 1986. Effect of genetically and environmentally induced heading date differences on yield and adaptation of an isogenic barley pair. *Crop Sci.* 26:889-893.

10. Wexelsen, H. 1934. Quantitative inheritance and linkage in barley. *Hereditas* 17:307-348.

Prepared:

J.D. Franckowiak and L.W. Gallagher. 1997. *Barley Genet. Newsl.* 26:101-102.

BGS 66, Six-rowed spike 1, *Vrs1.d*

Stock number: BGS 66  
Locus name: Six-rowed spike 1 (two-rowed spike)  
Locus symbol: *Vrs1.d* =  $V^d$

Previous nomenclature and gene symbolization:

Two-rowed barley or *Hordeum distichon* =  $V^d$  (5).  
Renamed *Vrs1.d* based on allelism tests.

Inheritance:

A partially dominant allele in the multiple allelic series at the *vrs1* (six-rowed spike 1) locus (4).

Located in chromosome 2HL (3); about 15.4 cM proximal from the *Gth1* (toothed lemma 1) locus (3); 30.5 cM from the *eog1* (elongated outer glume 1) locus (2).

Description:

Plants homozygous for *Vrs1.d* have more lateral kernels than those with *Vrs1.b* ( $V$ ) (5), which is the common allele in two-rowed barley. Homozygosity for the *Vrs1.d* allele and the *int-c.b* (formerly *i*) allele at the *int-c* (intermedium spike-c) locus prevents the development of ovules and awns in lateral spikelets. The *Vrs1.d* allele interacts with the *Int-c.a* (formerly *I*) allele to cause development of a few fertile lateral spikelets. Presence of the *Int-c.h* (formerly  $I^h$ ) allele contributes to a greater number of lateral kernels than *Int-c.a* (1).

Origin of mutant:

Natural occurrence in some two-rowed barley cultivars.

Mutational events:

*Vrs1.d* or  $V^d$  in Svanhals (PI 5474) (5).

Mutant used for description and seed stocks:

*Vrs1.d* or  $V^d$  (GSHO 346) in Svanhals; *Vrs1.d* is present in Bowman (PI 483237).

References:

1. Gymer, P.T. 1977. Probable allelism of *li* and *int-c* genes. Barley Genet. Newsl. 7:34-35.
2. Swenson, S.P., and D.G. Wells. 1944. The linkage relation of four genes in chromosome 1 of barley. J. Am. Soc. Agron. 36:429-435.
3. Wexelsen, H. 1934. Quantitative inheritance and linkage in barley. Hereditas 18:307-308.
4. Woodward, R.W. 1947. The  $I^h$ , *I*, *i* alleles in *Hordeum deficiens* genotypes of barley. J. Am. Soc. Agron. 39:474-482.
5. Woodward, R.W. 1949. The inheritance of fertility in the lateral florets of the four barley groups. Agron. J. 41:317-322.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:104.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:103.

BGS 67, Six-rowed spike 1, *Vrs1.t*

Stock number: BGS 67  
Locus name: Six-rowed spike 1 (deficiens spike)  
Locus symbol: *Vrs1.t*

Previous nomenclature and gene symbolization:

*Hordeum deficiens* =  $V^t$  (4).

Renamed *Vrs1.t* based on allelism tests.

Inheritance:

The *Vrs1.t* allele is the most dominant allele in the multiple allelic series at the *vrs1* (six-rowed spike 1) locus (4), but interacts as an incomplete dominant with some alleles.

Located in chromosome 2HL (1); about 15.4 cM distal from the *Gth1* (toothed lemma 1) locus (3); 30.5 cM distal from the *eog1* (elongated outer glume 1) locus (1).

Description:

Plants homozygous for *Vrs1.t* ( $V^t$ ) allele always have a deficiens phenotype regardless of the allele present at the *int-c* (intermedium spike-c) locus in chromosome 4H.

Deficiens is characterized by the extreme reduction in size of the lateral spikelet (4). The *Vrs1.t* allele in Engleawnless does not recombine with the *Lks1.a* allele at the *Lks1* (awnless) locus because a short paracentric inversion is present in this stock (2).

Origin of mutant:

Natural occurrence in two-rowed barleys previously classified as *Hordeum deficiens*.

Mutational events:

*Vrs1.t* or  $V^t$  in White Deficiens (CIho 7316, GSHO 684) (5).

Mutant used for description and seed stocks:

*Vrs1.t* or  $V^t$  in White Deficiens (GSHO 684); *Vrs1.t* in Bowman (PI 483237)\*8 (GSHO 1909, BW900, NGB 22332).

References:

1. Swenson, S.P., and D.G. Wells. 1944. The linkage relation of four genes in chromosome 1 of barley. J. Am. Soc. Agron. 36:429-435.
2. Tsuchiya, T., and R.J. Singh. 1972. Another case of paracentric inversion in a genetic stock, Engleawnless. Barley Genet. Newsl. 2:110-111.
3. Wexelsen, H. 1934. Quantitative inheritance and linkage in barley. Hereditas 18:307-308.
4. Woodward, R.W. 1947. The  $I^h$ ,  $I$ ,  $i$  alleles in *Hordeum deficiens* genotypes of barley. J. Am. Soc. Agron. 39:474-482.
5. Woodward, R.W. 1949. The inheritance of fertility in the lateral florets of the four barley groups. Agron. J. 41:317-322.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:105.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:104.

BGS 68, Purple veined lemma 1, *Pvc1*

Stock number: BGS 68  
Locus name: Purple veined lemma 1  
Locus symbol: *Pvc1*

Previous nomenclature and gene symbolization:

Purple veined lemma = C (1).  
Purple veined lemma =  $P_c$  (1).

Inheritance:

Monofactorial dominant (2), but Buckley suggested that three pairs of genes controlled expression of purple pigmentation of lemma veins (1).  
Located in chromosome 2HL (1, 2); about 22.2 cM distal from the *vrs1* (six-rowed spike 1) locus (1).

Description:

Purple pigment is produced by the presence of anthocyanins. When *Pv1c* is expressed, purple pigmentation of the kernel is confined mainly to the lemma veins (1). The pigments are formed late during grain fill when the lemma is exposed to sunlight, and they tend to fade as the spike matures.

Origin of mutant:

Natural occurrence in some cultivars and in some *Hordeum vulgare* subsp. *spontaneum* accessions.

Mutational events:

*Pvc1.a* (GSHO 132) in Buckley 2223-6 (1).

Mutant used for description and seed stocks:

*Pvc1.a* (GSHO 132) in Buckley 2223-6; *Pvc1.a* from R.I. Wolfe's Multiple Dominant Stock (GSHO 1565) in Bowman (PI 483237)\*7 (GSHO 1929, BW 651, NGB 22216).

References:

1. Buckley, G.F.H. 1930. Inheritance in barley with special reference to the color of caryopsis and lemma. *Sci. Agric.* 10:460-492.
2. Hayashi, J., R. Takahashi, and I. Moriya. 1977. A linkage of two complementary genes conditioning anthocyanin pigmentation in barley plants. *Nogaku Kenkyu* 56:167-178.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:108.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:105.

BGS 69, Toothed lemma 1, *Gth1*

Stock number: BGS 69  
Locus name: Toothed lemma 1  
Locus symbol: *Gth1*

Previous nomenclature and gene symbolization:

Toothed lemma = G (2, 5).

Inheritance:

Monofactorial dominant (3, 4).

Located in chromosome 2HL (2, 5); about 15.4 cM proximal from the *vrs1* (six-rowed spike 1) locus (1, 2, 5).

Description:

Large teeth or barbs are present on the upper part of lateral lemma nerves. The barbs are easiest to see on green spikelets. This trait may be difficult to study because Ubisch (4) reported three sizes of teeth, including one that could be seen only with magnification. According to Ubisch one gene pair controls the presence and absence of large teeth and one or two other genes are responsible for less developed teeth.

Segregation for only one pair of factors is reported by Wexelsen (5) and in subsequent studies.

Origin of mutant:

*Gth1.a* appears to be the normal allele, the recessive allele *gth1.b* is present in most two-rowed barley cultivars of Occidental origin.

Mutational events:

*Gth1.a* (GSHO 309) in Machine (Clho 4982) (5).

Mutant used for description and seed stocks:

*Gth1.a* (GSHO 309) in Machine; *Gth1.a* is present in Bowman (PI 483237); *gth1.b* from ND11894 in Bowman\*4 (GSHO 1897); *gth1.b* in Bowman\*6 (BW413, NGB 20646).

References:

1. Finch, R. A., and E. Simpson. 1978. New colours and complementary colour genes in barley. Z. Pflanzenzücht. 81:40-53.
2. Karpechenko, G.D., and K.V. Ivanova. 1932. Linkage of genes I and G in barley. Bull. Lab. Genet. Leningrad 9:97-108. [In Russian with English summary.]
3. Tschermak, E. von. 1901. Über Züchtung neuer Getreiderassen mittelst künstlicher Kreuzung. Kritisch-historische Betrachtungen. Zeitschrift für das landwirtschaftliche Versuchswesen Oesterreich 4:1029-1060.
4. Ubisch, G. von. 1919. Beitrag zu einer Faktorenanalyse von Gerste. II. Z. Indukt. Abstammungs. Vererbungs. 20:65-117.
5. Wexelsen, H. 1934. Q Quantitative inheritance and linkage in barley. Hereditas 18:307-348.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:109.

Revised:

T.E. Haus. 1978. Barley Genet. Newsl. 8:161.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:106.

BGS 70, Reaction to *Puccinia hordei* 1, *Rph1*

Stock number: BGS 70  
Locus name: Reaction to *Puccinia hordei* 1 (barley leaf rust)  
Locus symbol: *Rph1*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* = *Pa*<sub>1</sub> (9).  
Resistance to *Puccinia hordei* C = C (3).  
Resistance to *Puccinia hordei* Otth = *Pa* (3, 5).  
Resistance to *Puccinia hordei* Otth = *Rph1a* (4).

Inheritance:

Monofactorial incomplete dominant (2, 3).  
Located in chromosome 2H (7); probably in the short arm (6); associated with SNP markers 1\_0326 to 2\_1416 (positions 16.91 to 22.35 cM) in 2HS of the Bowman backcross-derived line BW682 (1), likely in 2H bin 02.

Description:

The seedling reaction type is 0;<sup>n</sup> - 1<sup>c</sup> with race 4 culture 57-19 (5); heterozygotes have reaction types ranging from 1 to 3, depending on parents (5, 6). Responses will vary for homozygotes and heterozygotes when different rust cultures are tested (6).

Origin of mutant:

Natural occurrence in Manchuria (Clho 2947) (2, 8).

Mutational events:

*Rph1.a* in Manchuria (Clho 2947) (5, 8); *Rph1.a* in Cape (PI 39403), OAC 21 (Clho 1470) (8); *Rph1.a* in Oderbrucker (Clho 940) (9); *Rph1.a* in Sudan (Clho 6489), Speciale (Clho 7536) (2, 5).

Mutant used for description and seed stocks:

*Rph1.a* in Oderbrucker (GSHO 1313); *Rph1.a* from Sudan in Bowman\*6 (PI 643150, BW682, NGB 22398).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic Dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp.110.166249.
2. Moseman, J.G., and C.W. Roane. 1959. Physiologic races of barley leaf rust (*Puccinia hordei*) isolated in the United States from 1956 to 1958. Plant Dis. Rep. 43:1000-1003.
3. Roane, C.W. 1962. Inheritance of reaction to *Puccinia hordei* in barley. I. Genes for resistance among North American race differentiating varieties. Phytopathology 52:1288-1295.
4. Roane, C.W. 1976. BGS 70, Resistance to *Puccinia hordei* Otth, *Rph1a*. BGN 6:120.
5. Roane, C.W., and T.M. Starling. 1967. Inheritance of reaction to *Puccinia hordei* in barley. II. Gene symbols for loci in different cultivars. Phytopathology 57:66-68.
6. Roane, C.W., and T.M. Starling. 1989. Linkage studies with genes conditioning leaf rust reaction in barley. Barley Newsl. 33:190-192.
7. Tuleen, N.A., and M.E. McDonald. 1971. Location of genes *Pa* and *Pa5*. Barley Newsl. 15:106-107.
8. Waterhouse, W.L. 1948. Studies in the inheritance of resistance to rust of barley, II. J. Proc. Royal Soc. New South Wales 81:198-205.
9. Watson, I.A., and F.C. Butler. 1947. Resistance to barley leaf rust (*Puccinia anomala* Rostr.). Linnean Soc. New South Wales, Proc. 72:379-386.



Prepared:

C.W. Roane. 1976. Barley Genet. Newsl. 6:120.

Revised:

J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:107.

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:52.

BGS 71, Compositum 2, *com2*

Stock number: BGS 71  
Locus name: Compositum 2  
Locus symbol: *com2*

Previous nomenclature and gene symbolization:

Branching inflorescent, rachilla 2 = *bir2* (3, 4).

Inheritance:

Monofactorial recessive (3, 6).

Located in chromosome 2HS (3, 4); associated with SNP markers 1\_0525 to 1\_0325 (positions 65.03 to 90.54 cM) in 2HS of the Bowman backcross-derived line BW192 and associated with markers 1\_0943 to 1\_1015 (positions 34.31 to 91.62 cM) in 2HS of the Bowman backcross-derived line BW187 (1); no SNP markers in 2HS were retained in the Bowman backcross-derived line BW191 (1), likely in 2H bin 06.

Description:

The spike is malformed because branch spikes fail to abort and rachis branches form from rachis nodes in the basal half of the spike. Spike branches form at more rachis nodes under favorable conditions for vigor growth (2, 5). Plants of the Bowman backcross-derived lines BW191 and BW192 were slightly shorter than Bowman and often had slightly shorter awns. Kernel sizes were variable for BW191 and BW192 and averages weights were lower than those of Bowman. Kernels were on average shorter and thinner, but BW191 plants had smaller grains than those of BW192. Grain yields of BW191 and BW192 were commonly lower than those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (6).

Mutational events:

*com2.f* (Mut 2201, GSHO 1700) in Donaria (PI 161974) (6); *com2.g* (GSHO 1703) from the ICARDA-CIMMYT collection of barley freaks (4); *com2.k* in Davis 1153 (GSHO 79), which likely is the same mutant as *com2.g* based on SNP markers retained in their Bowman backcross-derived lines (1).

Mutant used for description and seed stocks:

*com2.f* (GSHO 1700) in Donaria; *com2.f* in Bowman (PI 483237)\*7 (GSHO 2233, BW191, NGB 22023); *com2.g* in a freak stock from CIMMYT (GSHO 1703); *com2.g* in Bowman (PI 483237)\*8 (GSHO 1878, BW192, NGB 22024); *com2.k* in Davis 1153 (GSHO 79); *com2.k* in Bowman\*3 (BW187, NGB 22019). Based on marker retained in BW187 and BW192, the original donor parents might be identical.

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1992. Mapping a gene for photoperiod sensitivity in barley. Agron. Abstr. 1992:96.
4. Franckowiak, J.D. 1992. Allelism tests among selected semidwarf barleys. Barley Genet. Newsl. 21:17-23.
5. Franckowiak, J.D., B.P. Forster, U. Lundqvist, J. Lyon, I. Pitkethly, and W.T.B. Thomas. 2010. Developmental mutants as a guide to the barley phytomer. p. ?? In S. Ceccarelli and S. Grando. (eds.) Barley Genetics X. Proc. Tenth Int. Barley Genet. Symp., Alexandria, Egypt, 2008.

6. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l.l. Kulturpflanze 6:123-166.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:108.

Revised:

J. D. Franckowiak. 2010. Barley Genet. Newsl. 40:53-54.

BGS 72, Globosum-c, *glo-c*

Stock number: BGS 72  
Locus name: Globosum-c  
Locus symbol: *glo-c*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1, 3).

Located in chromosome 2H (3).

Description:

The kernels are more rounded or globe-shaped than in the parental cultivar. The spike is very lax with long rachis internodes (1).

Origin of mutant:

An X-ray induced mutant in Villa (PI 399506) (1).

Mutational events:

*glo-c.1004* (1080/72, GSHO 1329) in Villa (PI 399506) (1).

Mutant used for description and seed stocks:

*glo-c.1004* (GSHO 1329) in Villa; *glo-c.1004* in Bowman (PI 483237)\*4 (GSHO 1879);  
*glo-c.1004* in Bowman\*7 (BW394, NGB 20632).

References:

1. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
2. Häuser, H., and G. Fischbeck. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
3. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:109.

BGS 73, *Angustifolium-a*, *fol-a*

Stock number: BGS 73  
Locus name: *Angustifolium-a*  
Locus symbol: *fol-a*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1), but heterozygotes can be identified based on leaf width.  
Located in chromosome 2HL (1, 2); about 19.0 cM distal from the *vrs1* (six-rowed spike 1) locus (3).

Description:

Most organs are reduced in size. Plants have narrow, dark green leaves and a stunted, grassy growth habit (1, 2). Plant height is about 2/3 normal and spikes are 1/2 normal. Spikelets are about 2/3 normal size and the kernels are thin.

Origin of mutant:

An X-ray induced mutant in Proctor (PI 280420) (1, 2).

Mutational events:

*fol-a.1* (2235/64, GSHO 1744) in Proctor (PI 280420) (1, 2).

Mutant used for description and seed stocks:

*fol-a.1* (GSHO 1744) in Proctor; *fol-a.1* in Bowman (PI 483237)\*7 (GSHO 1927, BW370, NGB 20609).

References:

1. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
2. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.
3. Luna Villafañá, A. 1995. Mapping marker genes in chromosome 2 of barley. M.S. Thesis. North Dakota State Univ., Fargo.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:110.

BGS 74, Extra floret-c, *flo-c*

Stock number: BGS 74  
Locus name: Extra floret-c  
Locus symbol: *flo-c*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1, 3).

Located in chromosome 2HS (2); over 33.8 cM from the *Gth1* (toothed lemma 1) locus (2).

Description:

Extra bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra bracts is most common in the central portion of the spike, but rarely will the bracts form another spikelet.

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333) (3).

Mutational events:

*flo-c.5* (NGB 114275, GSHO 1743) in Foma (CIho 11333) (3).

Mutant used for description and seed stocks:

*flo-c.5* (GSHO 1743, NGB 114275) in Foma; *flo-c.5* in Bowman (PI 483237)\*7 (GSHO 1877, BW369, NGB 20608). (The *flo-c.5* mutant is likely an allele at the *flo-a* locus in 6HL.).

References:

1. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
2. Luna Villafañá, A. 1995. Mapping marker genes in chromosome 2 of barley. M.S. Thesis. North Dakota State Univ., Fargo.
3. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:111.

BGS 75, Awnless 1, *Lks1*

Stock number: BGS 75  
Locus name: Awnless 1  
Locus symbol: *Lks1*

Previous nomenclature and gene symbolization:

Awnless = *I* (Ikeno, see 3).  
Awnless = *Lk* (4).  
Awnless = *S* (8).  
Two-rowed awnless =  $V^{rk}$  (12).

Inheritance:

Monofactorial dominant (3, 4, 7).  
Located in chromosome 2HL (3, 4); about 9.6 cM distal from the *vrs1* (six-rowed spike 1) locus (8); *Lks1.a* is associated with SNP markers 1\_0619 to 1\_1533 (positions 133.59 to 141.56 cM) in 2H bins 09 to 10 of the Bowman backcross-derived line BW490 (2); *Lks1.b* is associated with SNP markers 2\_0667 to 1\_0287 (positions 117.73 to 138.37 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW491 (2), likely in 2H bin 09.

Description:

Little or no development of the appendage on the lemma occurs. Heterozygotes may be awnless (1) or awnletted (4) depending upon the source stock for the *Lks1* gene and the genetic background. The *Lks1.a* allele in Engleawnless will not recombine with alleles at the *vrs1* (six-rowed spike 1) locus (4, 13) because a short paracentric inversion is present in Engleawnless (14). The complex *vrs1* locus may include awnless and reduced awn length mutants (13). However, the *Lks1.b* gene in Clho 13311 does recombine with *vrs1* locus and is associated with a dominant instead of a recessive allele at the *Gth* (toothed lemma) locus (5). In the Atlas near-isogenic lines, the awnless trait reduced kernel weight by about 15% (9, 11) and grain yield by about 10% (9, 10, 11). Both backcross-derived lines, BW490 with *Lks1.a* and BW491 with *Lks1.b*, are slightly taller than Bowman. The kernels of BW490 are longer and thinner than those of Bowman and weighed about 25% less. The kernels of BW491 are similar in size to those of Bowman and weighed 5 to 10% less (5).

Origin of mutant:

Natural occurrence in Engleawnless or *Hordeum inerme* (Clho 2505, PI 174480) (3, 4); and several other accessions (4, 8).

Mutational events:

*Lks1.a* in Engleawnless (Clho 2505, GSHO 44) from England (1, 12, 14); *Lks1.b* in Clho 13311 (PI 316871, GSHO 1579) from Ethiopia; the dissimilar SNP marker haplotypes in the critical region of 2H suggests that the *Lks1* variants are of independent origin (2).

Mutant used for description and seed stocks:

*Lks1.a* in Engleawnless (GSHO 44); *Lks1.b* in Clho 13311 (PI 316871, GSHO 1579); *Lks1.a* from Clho 2505 in Betzes (PI 129430)\*7 (PI 534510); *Lks1.a* in Compana (PI 537442)\*7 (PI 534512); *Lks1.a* in Dekap (Clho 3351)\*7 (PI 534514); *Lks1.a* in Ingrid (Clho 10083)\*7 (PI 534516, Ridawn) (4); *Lks1.a* from Ridawn in Bowman (PI 483237)\*5 (GSHO 1913); in Bowman\*6 (BW490, NGB 20718); *Lks1.b* from Clho 13311 in Bowman\*6 (GSHO 1912); in Bowman\*7 (BW491, NGB 20719).

References:

1. Austenson, H.M. 1948. Linkage relations of the male sterile gene *ms<sub>2</sub>* in barley. M.S. Thesis. Univ. of Saskatchewan, Saskatoon.

2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Engledow, F.L. 1921. Inheritance in barley. II. The awn and the lateral floret. *J. Agric. Sci.* 11:159-196.
4. Engledow, F.L. 1924. Inheritance in barley. III. The awn and the lateral floret (cont'd): fluctuation: a linkage: multiple allelomorphs. *J. Genet.* 14:49-87.
5. Franckowiak, J.D. (Unpublished).
6. Hockett, E.A., and H.F. Bowman. 1990. Registration of awnless (short-awned) barley isogenic lines. *Crop Sci.* 30:754.
7. Huber, J.A. 1931. Vererbungsstudien an Gerstenkreuzungen. II. Zur Genetik der Gerstenähre. *Z. Zücht. A. Pflanzenzücht.* 16:394-464.
8. Kuckuck, H. 1930. Versuche einer vorläufigen Chromosomentopographie bei Gerste. *Züchter* 2:68-72.
9. Qualset, C.O., C.W. Schaller, and J.C. Wiloliams. 1965. Performance of isogenic lines of barley as influenced by awn length, linkage blocks, and environment. *Crop Sci.* 5:489-494.
10. Schaller, C.W., C.O. Qualset, and N. J. Rutger. 1972. Isogenic analysis of the effects of the awn on productivity of barley. *Crop Science* 12:531-535.
11. Schaller, C.W., and C.O. Qualset. 1975. Isogenic analysis of productivity in barley: Interaction of genes affecting awn length and leaf-spotting. *Crop. Sci.* 15:378-382.
12. Takahashi, R., J. Hayashi, I. Moriya, and S. Yasuda. 1982. Studies on classification and inheritance of barley varieties having awnless or short-awned lateral spikelets (Bozu barley). I. Variation of awn types and classification. *Nogaku Kenyu* 60:13-24. [In Japanese with English summary.]
13. Tsuchiya, T., and R.J. Singh. 1972. Another case of paracentric inversion in a genetic stock, Engleawnless. *Barley Genet. Newsl.* 2:110-111.
14. Wiebe, G.A. 1972. Tight linkage of the awnless gene in Engleawnless with the Vv locus. *Barley Genet. Newsl.* 2:108.

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:112.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:84-85.



BGS 76, Red lemma and pericarp 2, *Pre2*

Stock number: BGS 76  
Locus name: Red lemma and pericarp 2  
Locus symbol: *Pre2*

Previous nomenclature and gene symbolization:

Purple chaff color = *P* (1, 5).  
Purple chaff color = *P<sub>1</sub>* (8).  
Purple pericarp = *P* (3, 9, 11).  
Purple lemma = *P* (2).  
Red pericarp = *R* (2).  
Red pericarp 2 = *Re2* (10).

Inheritance:

Two dominant complementary genes (*Pre1* and *Pre2*) control purple or red pigmentation of the lemma, palea, and pericarp (2, 8, 12).  
Located in chromosome 2HL (2); about 17.1 cM distal from the *vrs1* (six-rowed spike 1) locus (2, 9, 12); over 11.2 cM proximal from the *ant2* (anthocyanin-less 2) locus (4, 6, 7).

Description:

Purple or red coloration of the hull (chaff) and pericarp develops during the soft dough stage of grain fill, and fades as the grain matures. Anthocyanin pigments in an acid cell solution produce the red to violet color observed in the pericarp and lemma (2).

Origin of mutant:

Natural occurrence in a few cultivars and some *Hordeum vulgare* subsp. *spontaneum* accessions (2, 12).

Mutational events:

*Pre2.a* in Buckley 3277 (NSL 32606, GSHO 234) (2).

Mutant used for description and seed stocks:

*Pre2.a* in Buckley 3277 (GSHO 234); *Pre2.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1565) in Bowman (PI 483237)\*9 (GSHO 1926, BW648, NGB 22213).

References:

1. Biffen, R.H. 1907. The hybridisation of barleys. J. Agric. Sci. 2:183-206.
2. Buckley, G.F.H. 1930. Inheritance in barley with special reference to the color of the caryopsis and lemma. Sci. Agric. 10:460-492.
3. Daane, A. 1931. Linkage relations in barley. Minn. Agric. Exp. Sta. Tech. Bull. 78. 30 p.
4. Doney, D.L. 1961. An inheritance and linkage study of barley with special emphasis on purple pigmentation of the auricle. M.S. Thesis. Utah State Univ., Logan.
5. Fraser, J.G.C. 1921. The dominant Mendelian characters in barley breeding. Sci. Agric. 2:113-116.
6. Heiner, R.E. 1958. Linkage and inheritance studies in barley. M.S. Thesis. Utah State Univ., Logan.
7. Imam, A.G.I. 1959. Inheritance and linkage studies in selected crosses of cultivated barley (*Hordeum vulgare* L.). M.S. Thesis. Utah State Univ., Logan.
8. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] Bot. Mag., Tokyo 36:25-38. [In Japanese.]
9. Myler, J.L., and E.H. Stanford. 1942. Color inheritance in barley. J. Am. Soc. Agron. 34:427-436.
10. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.
11. Ubisch, G. von. 1919. Beitrag zu einer Faktorenanalyse von Gerste. II. Z. Indukt.

Abstammungs. Vererbungs. 20:65-117.

12. Woodward, R.W., and J.W. Thieret. 1953. A genetic study of complementary genes for purple lemma, palea and pericarp in barley (*Hordeum vulgare* L.). Agron. J. 45:182-185.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:113-114.

BGS 77, Short culm 1, *hcm1*

Stock number: BGS 77  
Locus name: Short culm 1  
Locus symbol: *hcm1*

Previous nomenclature and gene symbolization:

Short culm = *h* (6).  
Short stature = *u* (1).

Inheritance:

Monofactorial recessive (1, 2, 5, 6).  
Located in chromosome 2HL (2); about 8.1 cM distal from the *eog1* (elongated outer glume 1) locus (5); closely linked in repulsion to the *Gth1* (toothed lemma 1) allele (5).

Description:

Plants homozygous for the *hcm1.a* allele average about 10 cm shorter than normal sibs. [Robertson et al. (4) assumed that the gene referred to as "uzu" by Miyake and Imai (1) and linked to six-rowed spike type (2, 3, 5, 6) were all the same, but allelism tests were conducted.] Linkage of the *hcm1.a* allele to the *vrs1.a* (six-rowed spike 1) allele is evident in many crosses of six- and two-rowed barley. The F<sub>1</sub>'s are taller than either parent and nearly all short segregates have a six-rowed spike. A slight increase in spike density (shorter rachis internodes) is observed in both homozygotes and heterozygotes when the *hcm1.a* allele is present. [The *Eam1* (early maturity 1) gene in Triple Bearded Mariout (BGS 57) makes the study of *hcm1.a* in certain environments difficult; therefore, changes in the seed stock and BGS number are recommended.]

Origin of mutant:

Natural occurrence in many six-rowed barley cultivars.

Mutational events:

*hcm1.a* in Triple Bearded Mariout (CIho 2523, GSHO 29) (5).

Mutant used for description and seed stocks:

*hcm1.a* in Morex (CIho 15773, GSHO 2492); *hcm1.a* is likely present in Bowman (PI 483237).

References:

1. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] Bot. Mag., Tokyo 36:25-38. [In Japanese.]
2. Neatby, R.W. 1929. An analysis of the inheritances of quantitative characters and linkage in barley. Sci. Agric. 9:701-718.
3. Powers, L. 1936. The nature of the interaction of genes affecting four quantitative characters in a cross between *Hordeum deficiens* and *vulgare*. Genetics 21:398-420.
4. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.
5. Swenson, S.P., and D.G. Wells. 1944. The linkage relation of four genes in chromosome 1 of barley. J. Am. Soc. Agron. 36:429-435.
6. Tedin, H., and O. Tedin. 1926. Contributions to the genetics of barley. I. Type of spike, nakedness and height of plant. Hereditas 7:151-160.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:102 as BGS 57, Short culm, *h*.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:115.

BGS 78, Mottled leaf 4, *mtt4*

Stock number: BGS 78  
Locus name: Mottled leaf 4  
Locus symbol: *mtt4*

Previous nomenclature and gene symbolization:

Mottled leaf-e = *mt<sub>e</sub>* (3).

Mottled leaf = *mt* (6).

Inheritance:

Monofactorial recessive (3, 4, 5).

Located in chromosome 2HL (3, 5); about 13.7 cM distal from the *vrs1* (six-rowed spike 1) locus (3, 5); *mtt4.e* is associated with SNP markers 2\_1340 to 2\_0182 (positions 166.06 to 185.53 cM) in 2H bins 11 to 12 of the Bowman backcross-derived line BW602 (1), likely in 2H bin 11.

Description:

When the plants are grown under cool conditions, white-yellowish blotches develop as horizontal bands in seedling leaves, 2 to 4 per leaf blade (3). The bands faded as the plant grows or under warmer environmental conditions. At later stages of development, plants had a slightly yellow-green color (2). Plants of the Bowman backcross-derived line for *mtt4.e*, BW602, headed a few days later than Bowman, had 2 to 3 more kernels per spike, were slightly shorter, had slightly lighter kernel weights. The grain yields of BW602 were similar to those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Victorie (OUU010, Clho 5077) (3).

Mutational events:

*mtt4.e* (OUL076, GSHO 1231) in Victorie (3).

Mutant used for description and seed stocks:

*mtt4.e* in Victorie (GSHO 1231, OUL076); *mtt4.e* in Bowman (PI 483237)\*6 (GSHO 1914); *mtt4.e* in Bowman\*7 (BW602, NGB 22168).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VI. Ten mutant genes located on chromosomes 1 to 7, except 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:227-250.
4. Takahashi, R., J. Hayashi, and I. Moriya. 1972. New linkage data obtained in 1971. *Barley Genet. Newsl.* 2:74-76.
5. Takahashi, R., J. Hayashi, and I. Moriya. 1974. New linkage data obtained during 1972-73 season. *Barley Genet. Newsl.* 4:74-76.
6. Tsuchiya, T. 1974. Linkage maps of barley as of March 1974. *Barley Genet. Newsl.* 4:126-130.

Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:116.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:86.

BGS 79, White streak 7, *wst7*

Stock number: BGS 79  
Locus name: White streak 7  
Locus symbol: *wst7*

Previous nomenclature and gene symbolization:

Ribbon grass = *rb* (7).

White streak-k = *wst*,*k* (11).

White streak-B = *wst*,*B* (9).

Inheritance:

Monofactorial recessive (2, 12).

Located in chromosome 2HL (6, 8, 9, 10); about 22.0 cM distal from the *gpa1* (grandpa 1) locus (2, 10); over 29.4 cM distal from the *lig1* (liguleless 1) locus (9); about 6.1 cM from RFLP marker MWG949A (1); *wst7.k* is associated with SNP markers 2\_1346 and 1\_283 (positions 233.94 and 234.63 cM) in 2H bin 14 of the Bowman backcross-derived line BW916 (3), in 2H bin 14.

Description:

Vertical white streaks of variable width and number develop in the leaf blades of young secondary tillers. Fewer white streaks and fewer tillers with white streaks occur as environmental conditions become warm. White streaks can be found until near maturity, but they are difficult to observe after heading under field conditions. Often the lower or first leaves on early tillers have more and wider streaks. There were no apparent effects of the *wst7.k* gene on agronomic traits in the Bowman backcross-derived line BW916 (5).

Origin of mutant:

A spontaneous mutant isolated by Robertson (7, 12).

Mutational events:

*wst7.k* (GSHO 247) in an unknown cultivar (2, 12).

Mutant used for description and seed stocks:

*wst7.k* in an unknown cultivar (GSHO 247); *wst7.k* from R.I. Wolfe's Multiple Recessive Marker Stock (GSHO 3451) in Bowman (PI 483237)\*7 (GSHO 1935, BW916, NGB 22347).

References:

1. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. *Theor. Appl. Genet.* 103:415-424.
2. Doney, D.L. 1961. An inheritance and linkage study of barley with special emphasis on purple pigmentation or the auricle. M.S. Thesis. Utah State Univ., Logan.
3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
4. Franckowiak, J.D. 1996. Coordinator's report: Chromosome 2. *Barley Genet. Newsl.* 25:88-90.
5. Franckowiak, J.D. (Unpublished).
6. Kasha, K.J. 1982. Coordinator's report: Chromosome 6. *Barley Genet. Newsl.* 12:90-92.
7. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. *J. Am. Soc. Agron.* 39:464-473.
8. Schondelmaier, J., G. Fischbeck, and A. Jahoor. 1993. Linkage studies between

- morphological and RFLP markers in the barley genome. Barley Genet. Newsl. 22:57-62.
9. Shin, J.S., S. Chao, L. Corpuz, and T.K. Blake. 1990. A partial map of the barley genome incorporating restriction fragment length polymorphism, polymerase chain reaction, isozyme, and morphological marker loci. Genome 23:803-810.
10. Walker, G.W.R. 1974. Linkage data for *rb* and *mt3*. Barley Genet. Newsl. 4:90-91.
11. Wolfe, R.I., and J.D. Franckowiak. 1991. Multiple dominant and recessive genetic marker stocks in spring barley. Barley Genet. Newsl. 20:117-121.
12. Woodward, R.W. 1957. Linkages in barley. Agron. J. 49:28-32.

Prepared:

J.D. Franckowiak and R.I. Wolfe. 1997. Barley Genet. Newsl. 117.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:207-208.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:87-88.

BGS 80, Anthocyanin-less 2, *ant2*

Stock number: BGS 80  
Locus name: Anthocyanin-less 2  
Locus symbol: *ant2*

Previous nomenclature and gene symbolization:

Non-purple straw = *p<sub>r</sub>* or *pr* (6).  
Anthocyanin-less = *ant-2* (1, 4).  
Exrubrum = *rub* (2).  
Colorless leaf tip 2 = *clt<sub>2</sub>* (3), *c<sub>2</sub>* (3).

Inheritance:

Monofactorial recessive (1, 6).  
Located in chromosome 2HL (1, 6); about 15.1 cM distal from the *vrs1* (six-rowed spike 1) locus (6, 7, 8).

Description:

Anthocyanin pigments are not observed in any vegetative plant parts, including the stem, auricles, lemma, and awn (1, 3, 4). The straw does not develop a purple pigmentation as it approaches maturity (6). The recommended symbol for the dominant allele is *Ant2.c* (formerly *Pr*).

Origin of mutant:

Natural occurrence in few cultivars (5, 6), the first 3 or 4 natural occurrences may be the same allele.

Mutational events:

*ant2.d* (*pr1.b*) in Alva (NSGC1866), *ant2.e* (*pr1.c*) in Balder (PI 195481), *ant2.f* (*pr1.d*) in Cambrinus (PI 321779), *ant2.g* (*pr1.e*) in Sultan (PI 339814) (5); *ant2.15* (NGB 114564), 2.20 (NGB 114569, GSHO 1632), 2.23 (NGB 114572), 2.25 (NGB 114575), 2.26 (NGB 114576), 2.27 (NGB 114278) in Foma (CIho 11333) (4); *ant2.41* (NGB 114596) in Mari (CIho 11334), 2.46 (NGB 111505) in Foma, 2.47 (NGB 111823), 2.48 (NGB 111782), 2.49 (NGB 111808), 2.50 (NGB 111811), 2.51 (NGB 111817), 2.54 (NGB 111872), 2.55 (NGB 111787) in Bonus (PI 189763), 2.112, 2.113, 2.114, 2.115, 2.116, 2.117, 2.118, 2.120, 2.121, 2.122, 2.130 in Nordal (5); *ant2.h* (*pr1.f*) in Shyri (GSHO 2430).

Mutant used for description and seed stocks:

*ant2.20* in Foma (NGB 114569, GSHO 1632); *ant2.h* from Shyri in Bowman (PI 483237)\*5 (GSHO 1919); *ant2.h* in Bowman\*7 (BW020, NGB 20428); *ant2.20* in Bowman\*2 (GSHO 1920); *ant2.20* in Bowman\*6 (BW019, NGB 20427).

References:

1. Finch, R.A., and E. Simpson. 1978. New colours and complementary colour genes in barley. *Z. Pflanzenzücht.* 81:40-53.
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
3. Hayashi, J., R. Takahashi, and I. Moriya. 1977. A linkage study of two complementary genes conditioning anthocyanin pigmentation in barley plants. *Nogaku Kenkyu* 56:167-178.
4. Jende-Strid, B., and U. Lundqvist. 1978. Diallelic tests of anthocyanin-deficient mutants. *Barley Genet. Newsl.* 8:57-59.
5. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:76-79.
6. Robertson, D.W. 1933. Inheritance in barley. *Genetics* 18:148-158.
7. Takahashi, R., J. Hayashi, and I. Moriya. 1971. Linkage studies in barley. *Barley Genet. Newsl.* 1:51-58.

8. Woodward, R.W. 1957. Linkages in barley. *Agron. J.* 49:28-32.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:107 as BGS 53, Purple straw, *Pr.*

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:118.



BGS 81, Glossy sheath 7, *gsh7*

Stock number: BGS 81  
Locus name: Glossy sheath 7  
Locus symbol: *gsh7*

Previous nomenclature and gene symbolization:

Glossy sheath 7 = *gs7* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosomes 1H, 2HL or 5H (1); based on segments of the donor parent chromosomes retained in the Bowman backcross-derived line BW410, possible locations based on SNP markers included 1\_0259 to 2\_0229 (positions 70.78 to 106.61 cM) in 1H, 1\_0916 to 2\_0681 (positions 187.68 to 247.86 cM) in 2HL, 1\_0580 to 1\_0955 (positions 54.27 to 69.76 cM) in 5HS, and 2\_0367 to 2\_1445 (positions 116.66 to 134.85 cM) in 5HL (1).

Description:

The spike, leaf sheath and stem of mutant plants are glossy and bright green in color (wax code - - ++ ) (3). In early generation backcrosses to Bowman, the glossy sheath 7 segregates headed early and had poor vigor and small spikes. Also, spikes frequently abort after emasculation (2). Plants of the Bowman backcross-derived line were 2/3 to 3/4 of normal height. Kernels are slightly longer and thinner than those of Bowman and kernel weights are about 2/3 of normal. Grain yields are less than 10% of normal (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (3).

Mutational events:

*gsh7.ae* (GSHO 1759) in Akashinriki (OUM022) (3).

Mutant used for description and seed stocks:

*gsh7.ae* in Akashinriki (GSHO 1759); *gsh7.ae* in Bowman (PI 483237)\*5 (GSHO 2269, BW410, NGB 20643).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:119.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:55.

BGS 82, Zeocriton 1, *Zeo1*

Stock number: BGS 82  
Locus name: Zeocriton 1  
Locus symbol: *Zeo1*

Previous nomenclature and gene symbolization:

Erectoides-52 = *ert-52* (6, 7).  
Erectoides-r = *Ert-r* (10).  
"Kurz und dicht" = *Knd* (12, 14).

Inheritance:

Monofactorial incomplete dominant (6, 11).  
Located in chromosome 2HL (9); about 9.2 cM distal from the *lig1* (liguleless 1) locus (9); about 7.3 cM distal from RFLP marker *cnx1* in 2H bin 13 (1); the *Ert-r.52* allele in Bowman backcross-derived line BW322 is associated with SNP markers 2\_0715 to 1\_0551 (positions 213.08 to 221.70 cM) in 2H bin 13 (2); the *Zeo1.a* allele in BW937 is associated with SNP markers 2\_0715 to 2\_1453 (positions 213.08 to 245.71 cM) in 2H bin 13/14 (2); the *Zeo1.b* allele in BW938 is associated with SNP markers 1\_1486 to 2\_0590 (positions 202.70 to 218.47) in 2H bin 13 (2), likely in 2H bin 13.

Description:

Plants heterozygous for *Zeo1* have short culms, compact spikes, and wide kernels. Homozygotes have shorter culms (short peduncle), very compact spikes, large outer glumes with long awns, and reduced fertility (14). Generally, the spike emerges from the side of the sheath in homozygotes. Although the name *zeocriton* is used for this gene, this gene is not from Spratt, the dense ear type described by Engledow (3) or those described by Hayes and Harlan (8). Spikes of plants with the *Ert-r.52* mutant are compact in heterozygotes and very compact in homozygotes, with rachis internode length values from 1.4 to 1.8 mm. Homozygotes are about 2/3 normal height with excellent vigor. The glumes associated with lateral spikelets are 3 to 4 times larger than normal. Lodicule size is reduced (11). Heterozygotes are intermediate in plant height, have slightly more lax spikes, and have normal glumes in lateral spikelets (11). GA<sub>3</sub> treatment of plants as the flag leaf emerges decreases spike density (13). Plants in Bowman backcross lines for *Ert-r.52* (BW322), *Zeo1.a* (BW937), and *Zeo1.b* (BW938) are about 2/3 the height of Bowman. Rachis internodes are about 1/2 normal length (2.2 vs. 4.4 mm). Mutant plants head about two days later than Bowman; they have about 2 more kernels per spike and their grain yields are about 3/4 of those of Bowman. Plants with *Ert-r.52* mutant appear slightly less stunted than those with *Zeo1.a* or *Zeo1.b* (5). The *Zeo1* locus is very close to the *Zeo2* locus (2, 5).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (12); a neutron induced mutant in Bonus (PI 189763) (6).

Mutational events:

*Zeo1.a* in Donaria (Mut 2657, GSHO 1613) (12); *Zeo1.b*, received as "Kurz und dicht" and placed in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614) (4, 14); *Ert-r.52* (NGB 112651, GSHO 492), *-r.67* (NGB 112666) in Bonus, *-r.329* (NGB 112844) in Foma (CIho 11333) (11); *Ert-r.453* (NGB 112968) in Foma (10).

Mutant used for description and seed stocks:

*Zeo1.a* in Donaria (GSHO 1613); *Zeo1.a* in Bowman (PI 483237)\*5 (GSHO 1931), in Bowman\*7 (BW937, NGB 22366); *Zeo1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614) in Bowman\*9 (GSHO 1932, BW938, NGB 22367); *Ert-r.52* in Bonus (GSHO 492, NGB 112651); *Ert-r.52* in Bowman (PI 483237)\*8 (GSHO 2123, BW322,

NGB 22117).

References:

1. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szücs, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. *Theor. Appl. Genet.* 103:415-424.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
3. Engledow, F.L. 1924. Inheritance in barley. III. The awn and the lateral floret (cont'd): fluctuation: a linkage: multiple allelomorphs. *J. Genet.* 14:49-87.
4. Franckowiak, J.D. 1992. Allelism tests among selected semidwarf barleys. *Barley Genet. Newsl.* 21:17-23.
5. Franckowiak, J.D. (Unpublished).
6. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
7. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) *Recent Plant Breeding Research. Svalöf 1946-1961.* Almquist & Wiksell, Stockholm.
8. Hayes, H.K., and H.V. Harlan. 1920. The inheritance of the length of internode in the rachis of the barley spike. U.S. Dept. Agr., Bull. 869. 26 pp.
9. Luna Villafañá, A., and J.D. Franckowiak. 1995. (Unpublished).
10. Lundqvist, U., and J.D. Franckowiak. 1997. BGS 332, Erectoides-r, *Ert-r*. *Barley Genet. Newsl.* 26:280.
11. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.
12. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. I. Kulturpflanze 6:123-166.
13. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.
14. Wolfe, R.I. (Unpublished).

Prepared:

J.D. Franckowiak and R.I. Wolfe. 1997. *Barley Genet. Newsl.* 26:120.  
 U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:280. as BGS 332, Erectoides-r, *Ert-r*.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:209.  
 J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:89-90.

BGS 83, Slender dwarf 2, *sld2*

Stock number: BGS 83  
Locus name: Slender dwarf 2  
Locus symbol: *sld2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HS (2); over 18.2 cM distal from the *eog1* (elongated outer glume 1) locus (2).

Description:

Mutant plants have short and slender culms, narrow leaves, short and lax spikes, and thin kernels (2). When grown at Langdon, North Dakota, USA, semi-dwarf plants are difficult to identify in progenies from crosses between OUM142 and two-rowed spring barley. The frequency of semidwarf, late maturing plants is low because *sld2.b* is linked to an *Eam1* (early maturity 1) gene in the repulsion phase (1).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (2).

Mutational events:

*sld2.b* (OUM142, GSHO 2491) in Akashinriki (OUJ659, PI 467400) (2).

Mutant used for description and seed stocks:

*sld2.b* (GSHO 2491, OUM 142) in Akashinriki; *sld2.b* in Bowman (PI 483237)\*4 (GSHO 1876); *sld2.b* in Bowman\*7 (BW862, NGB 22299).

References:

1. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
2. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VI. Ten mutant genes located on chromosomes 1 to 7, except 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:227-250.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:121.

BGS 84, Midseason stripe 1, *mss1*

Stock number: BGS 84  
Locus name: Midseason stripe 1  
Locus symbol: *mss1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2), the deviation from 3:1 reported by Walker et al (1) may be caused by genotype-environment interactions.

Located in chromosome 2H (1, 2); about 19.9 cM distal (probably) from the *vrs1* (six-rowed spike 1) locus (1).

Description:

Broad yellow to ivory vertical streaks develop in the leaves of some tillers prior to heading (1, 2). Affected tillers are weaker and often abort under moderate to severe heat or moisture stress. In some environments, the whole plant becomes a golden yellow prior to maturation.

Origin of mutant:

A gamma-ray induced mutant in Montcalm (Clho 7149) (2).

Mutational events:

*mss1.a* (Alb Acc 257, GSHO 1404) in Montcalm (Clho 7149) (1, 2).

Mutant used for description and seed stocks:

*mss1.a* (GSHO 1404) in Montcalm; *mss1.a* in Bowman (PI 483237)\*2 (GSHO 1918);

*mss1.a* in Bowman\*6 (BW593, NGB 22159).

References:

1. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.
2. Walker, G.W., K. Kasha, and R.A. Miller. 1958. Recombination studies in barley. Proc. Genet. Soc. Can. 3:41-43.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:122.

BGS 85, Yellow streak 4, *yst4*

Stock number: BGS 85  
Locus name: Yellow streak 4  
Locus symbol: *yst4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HL (2); near the *vrs1* (six-rowed spike 1) locus (2), in bin 2H-07 near RFLP marker CDO537 (3).

Description:

Plants have a yellow-green color with numerous, vertical yellow streaks in the leaves. The yellow-green color is retained until maturity, but the yellow streaks may be difficult to observe after heading. Plant vigor and height are reduced, heading is delayed, and seed yields are low.

Origin of mutant:

A sodium azide induced mutant in Glenn (CIho 15769) (1).

Mutational events:

*yst4.d* (DWS1059, GSHO 2502) in Glenn (CIho 15769) (2).

Mutant used for description and seed stocks:

*yst4.d* in Glenn (GSHO 2502); *yst4.d* in Bowman (PI 483237)\*7 (GSHO 1922, BW927, NGB 22476).

References:

1. Faue, A.C. 1987. Chemical mutagenesis as a breeding tool for barley. M.S. Thesis. North Dakota State Univ., Fargo.
2. Faue, A.C., A.E. Foster, and J.D. Franckowiak. 1989. Allelism testing of an induced yellow streak mutant with the three known yellow streak mutants. Barley Genet. Newsl. 19:15-16.
3. Kleinhofs, A. 2002. Integrating molecular and morphological/physiological marker maps. Coordinator's Report. Barley Genet. Newsl. 32:152-159.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:123.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:210.

BGS 86, Chlorina seedling 13, *fch13*

Stock number: BGS 86  
Locus name: Chlorina seedling 13  
Locus symbol: *fch13*

Previous nomenclature and gene symbolization:

Chlorina seedling 13 = *f13* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The mutant is classified as white seedlings (devoid of chlorophyll and carotenoid pigments) and a heterozygous stock is maintained in the USDA-ARS Barley Genetic Stocks Collection. Mutant plants die at the seedling stage if planted in the field. When grown in the greenhouse, however, seedlings gradually develop a pale green color, leaves have a light green color at heading, and plants survive to maturity and produce plump seed (1).

Origin of mutant:

A spontaneous mutant in Nigrinudum (NSL 3286, GSHO 988) (1).

Mutational events:

*fch13.v* (Nigrinudum II, GSHO 16) in Nigrinudum (NSL 3286, GSHO 988) (1).

Mutant used for description and seed stocks:

*fch13.v* (GSHO 16) in Nigrinudum; *fch13.v* in Bowman (PI 483237)\*6 (BW355, NGB 20594).

References:

1. Hang, A. 1993. Trisomic analysis on the chlorina mutant B2-4. Barley Genet. Newsl.22:23-24.

Prepared:

A. Hang and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:124.

BGS 87, Chlorina seedling 14, *fch14*

Stock number: BGS 87  
Locus name: Chlorina seedling 14  
Locus symbol: *fch14*

Previous nomenclature and gene symbolization:

Chlorina seedling 14 = *f14* (2).

Inheritance:

Monofactorial recessive (2, 4).

Located in chromosome 2HL (2); probably between the *vrs1* (six-rowed spike 1) and the *ant2* (anthocyanin-less 2) loci (2), likely in 2H bin11 (3, 4).

Description:

Seedlings have a pale yellow-green color. The leaves gradually become greener starting at the tip of the leaf blade, and mutant plants are indistinguishable in color from normal sibs at heading (2). When grown in the field, plants produce slightly thinner kernels with about a 10% reduction in kernel weight (1).

Origin of mutant:

A spontaneous mutant in Shyri (GSHO 2430, Lignee 640//Kober/Teran 78) from Ecuador (2).

Mutational events:

*fch14.w* (GSHO 1739) in Shyri (GSHO 2430) (2, 5).

Mutant used for description and seed stocks:

*fch14.w* in Shyri (GSHO 1739); *fch14.w* in Bowman (PI 483237)\*6 (GSHO 1911, BW356, NGB 20595).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
3. Kleinhofs, A. 2006. Integrating molecular and morphological/physiological marker maps. *Barley Genet. Newsl.* 36:66-82.
4. Kudrna, D., A. Kleinhofs, A. Kilian, and J. Soule. 1996. Integrating visual markers with the Steptoe x Morex RFLP map. p. 343. *In* A.E. Slinkard, G.J. Scoles, and B.G. Rossnagel (eds.) *Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp.*, Saskatoon. Univ. of Saskatchewan, Saskatoon.
5. Rivendeneira, M. (Personal communications).

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:125.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:211.



BGS 88, Reaction to *Puccinia hordei* 2, *Rph2*

Stock number: BGS 88  
Locus name: Reaction to *Puccinia hordei* 2 (barley leaf rust)  
Locus symbol: *Rph2*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia anomala* Rostr = *Pa* (2).  
Resistance to *Puccinia hordei* Otth 2 = *Pa*<sub>2</sub> (9, 15).  
Resistance to *Puccinia hordei* A = *A* (8, 9).

Inheritance:

Monofactorial incomplete dominant (2, 14).  
Located in chromosome 5HS (1); not in the long arm (10); distal from the secondary constriction (1); about 3.5 cM proximal from RFLP marker CDO749 in 5H bin 04 (1).

Description:

The seedling reaction type is 0<sup>n</sup> - 1<sup>c</sup> with race 4 culture 57-19 (2); heterozygotes have reaction types ranging from 1 to 3, depending on parents. Responses will vary for homozygotes and heterozygotes when different rust cultures are tested (8).

Origin of mutant:

Natural occurrence in Peruvian (CIho 935) and several other cultivars (2, 4, 6, 12, 15, 16).

Mutational events:

*Rph2.b* in Peruvian (4, 12); *Rph2.j* in Batna (CIho 3391) (7, 12); *Rph2.k* in Weider (No 22, PI 39398) (2, 11, 15); *Rph2.l* in Juliaca (PI 39151) (3, 12); *Rph2.m* in Kwan (PI 39367, GSHO 1392) (2, 4, 12); *Rph2.n* in Chilean D (PI 48136) (4, 14); an allele at the *Rph2* locus is present in Purple Nepal (CIho 1373), Modia (CIho 2483), Morocco (CIho 4975), Barley 305 (CIho 6015), Marco (PI 94877) (2); Austral (CIho 6358) (4, 6, 7, 12); Marocaine 079 (CIho 8334) (6); Q21861 (PI 584766), TR306 (1, 13); accessions with a second *Rph* gene besides the *Rph2* allele include Carre 180 (CIho 3390), CIho 14077 (12); Ricardo (PI 45492) (2, 14, 16); Ariana (CIho 14081) (11, 12, 16); Quinn (PI 39401) (8, 9); Bolivia (PI 36360) (2, 8, 9); Reka 1 (CIho 5051) (4, 6, 7, 12); tentative *Rph2* allele symbols are *Rph2.q* in Quinn, *Rph2.r* in Bolivia (GSHO 1598), *Rph2.s* in Ricardo, *Rph2.t* in Reka 1 (GSHO 1594), and *Rph2.u* in Ariana based on differential reactions and different cultivar origins (5, 8, 9, 12); *Rph2.y* from HJ198\*3/HS2310 (PI 531841, GSHO 1595) (3).

Mutant used for description and seed stocks:

*Rph2.b* in Peruvian (GSHO 1593); *Rph2.b* from Peruvian in Bowman (PI 483237)\*3 (GSHO 2320, PI 643151, BW737, NGB 22443); *Rph2.j* from Batna in Bowman\*6 (PI 643165, BW738, NGB22444); *Rph2.l* from Juliaca in Bowman\*4 (BW739, NGB 22445); *Rph2.r* from Bolivia in Bowman\*5 (BW742, NGB 22448); *Rph2.t* from Rika 1 in Bowman\*8 (GSHO 2321, PI 643167, BW 743, NGB 22449); *Rph2.y* from PI 531841 in Bowman\*5 (PI 643166, BW744, NGB 22450).

References

1. Borovkova, I.G., Y. Jin, B.J. Steffenson, A. Kilian, T.K. Blake, and A. Kleinhofs. 1997. Identification and mapping of a leaf rust resistance gene in the barley line Q21861. *Genome* 40:236-241.
2. Henderson, M.T. 1945. Studies of the sources of resistance and inheritance of reaction to leaf rust, *Puccinia anomala* Rostr., in barley. Ph.D. Thesis. Univ. of Minnesota, St. Paul.
3. Jin, Y., G.H. Cui, B.J. Steffenson, and J.D. Franckowiak. 1996. New leaf rust resistance genes in barley and their allelic and linkage relationships with other *Rph*

genes. *Phytopathology* 86:887-890.

4. Levine, M.N., and W.J. Cherewick. 1952. Studies on dwarf leaf rust of barley. U.S. Dept. Agr. Tech. Bull. 1056. 17p.

5. Moseman, J.G., and L.W. Greeley. 1965. New physiological strains of *Puccinia hordei* among physiological races identified in the United States from 1959 through 1964. *Plant Dis. Rep.* 49:575-578.

6. Moseman, J.G., and C.W. Roane. 1959. Physiologic races of barley leaf rust (*Puccinia hordei*) isolated in the United States from 1952 to 1958. *Plant Dis. Rep.* 43:1000-1003.

7. Reinhold, M., and E.L. Sharp. 1982. Virulence types of *Puccinia hordei* from North America, North Africa and the Middle East. *Plant. Dis.* 66:1009-1011.

8. Roane, C.W. 1962. Inheritance of reaction to *Puccinia hordei* in barley. I. Genes for resistance among North American race differentiating varieties. *Phytopathology* 52:1288-1295.

9. Roane, C.W., and T.M. Starling. 1967. Inheritance of reaction to *Puccinia hordei* in barley. II. Gene symbols for loci in different cultivars. *Phytopathology* 57:66-68.

10. Roane, C.W., and T.M. Starling. 1989. Linkage studies with genes conditioning leaf rust reaction in barley. *Barley Newsl.* 33:190-192.

11. Sharp, E.L., and M. Reinhold. 1982. Resistance gene sources to *Puccinia hordei* in barley. *Plant Dis.* 66:1012-1013.

12. Starling, T.M. 1955. Sources, inheritance, and linkage relationships of resistance to race 4 of leaf rust (*Puccinia hordei* Otth), race 9 of powdery mildew (*Erysiphe graminis hordei* El. Marchal), and certain agronomic characters in barley. *Iowa State Coll. J. Sci.* 30:438-439.

13. Steffenson, B.J., and Y. Jin. 1997. A multi-allelic series at the *Rph2* locus for leaf rust resistance in barley. *Cereal Rusts Powdery Mildews Bull.* (in press).

14. Tan, B.H. 1977. Evaluation host differentials of *Puccinia hordei*. *Cereal Rust Bull.* 5:17-23.

15. Watson, I.A., and F.C. Butler. 1947. Resistance to barley leaf rust (*Puccinia anomala* Rostr.). *Linnean Soc. New South Wales, Proc.* 72:379-386.

16. Zloten, R.R. 1952. The inheritance of reaction to leaf rust in barley. M.S. Thesis. Univ. of Manitoba, Winnipeg.

Prepared:

Y. Jin and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:126-127.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:212-213.

BGS 89, Breviaristatum-g, *ari-g*

Stock number: BGS 89  
Locus name: Breviaristatum-g  
Locus symbol: *ari-g*

Previous nomenclature and gene symbolization:

Breviaristatum-18 = *ari-18* (2, 3).  
Short awn 10 = *lk10* (5).

Inheritance:

Monofactorial recessive (3).  
Located in chromosome 2H (1); the linkage drag association with the *Gth1* (toothed lemma 1) locus (1) may be caused by poor expression of the *Gth1.a* allele in the Bowman backcross-derived line.

Description:

Plants are semidwarf and very weak. Awns are 1/4 to 1/3 normal and stiff, spikes are short and small, and seed set is low. Leaf blades are very narrow and often involuted (3). When grown in the field at Fargo, North Dakota, USA, plant development is very slow, the upper portion of the sheath is white as new leaves emerge, and spikes are seldom produced.

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

*ari-g.18* (NGB 115865) in Bonus (PI 189763) (3); *ari-g.24* (NGB 115872, GSHO 1655) in Bonus (4); *ari-g.134* (NGB 115944), *-g.138* (NGB 115948), *-g.142* (NGB 115952), *-g.158* (NGB 115968), *-g.221* (NGB 116030), *-g.234* (NGB 116044), *-g.246* (NGB 116056) in Foma (CIho 11333), *-g.267* (NGB 116078) in Kristina (NGB 1500) (3); *ari-g.303* (NGB 116127) in Kristina (4).

Mutant used for description and seed stocks:

*ari-g.24* in Bonus (NGB 115872, GSHO 1655); *ari-g.24* in Bowman (PI 483237)\*7 (GSHO 2503); *ari-g.24* in Bowman\*8 (BW045, NGB 20453).

References:

1. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
3. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
4. Lundqvist, U. (Unpublished).
5. Tsuchiya, T. 1974. Allelic relationships of genes for short-awned mutants in barley. Barley Genet. Newsl 4:80-81.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:128.

BGS 90, Erectoides-j, *ert-j*

Stock number: BGS 90  
Locus name: Erectoides-j  
Locus symbol: *ert-j*

Previous nomenclature and gene symbolization:

Erectoides-31 = *ert-31* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2H (1); based on linkage drag with the *Gth1* (toothed lemma 1) locus (1).

Description:

Spikes are semicompact with rachis internode length estimates of 2.4 and 2.6 mm, and culms are about 3/4 normal length (5).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

*ert-j.31* (NGB 112632, GSHO 484) in Bonus (PI 189763) (2); *ert-j.74* (NGB 112673) in Bonus (3); *ert-j.326* (NGB 112841) in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

*ert-j.31* in Bonus (NGB 112632, GSHO 484); *ert-j.31* in Bowman (PI 483237)\*7 (GSHO 1902, BW313, NGB 22109).

References:

1. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
2. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
3. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. In E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
4. Lundqvist, U. (Unpublished).
5. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:129.

BGS 91, Erectoides-q, *ert-q*

Stock number: BGS 91  
Locus name: Erectoides-q  
Locus symbol: *ert-q*

Previous nomenclature and gene symbolization:

Erectoides-101 = *ert-101* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2H (1); based on linkage drag with the *Gth1* (toothed lemma 1) locus (1).

Description:

Spikes are semicompact and have slightly irregular placement of kernels. Seedlings leaves are slightly wider than normal, awns are about 3/4 normal length, and plants are semidwarf (3/4 of normal culm length).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (3).

Mutational events:

*ert-q.101* (NGB 112700, GSHO 1562) in Bonus (PI 189763) (3); *ert-q.392* (NGB 112909, GSHO 491), *-q.421* (NGB 112937) in Foma (CIho 11333) (2).

Mutant used for description and seed stocks:

*ert-q.101* in Bonus (NGB 112700, GSHO 1562); *ert-q.101* in Bowman (PI 483237)\*7 (GSHO 1903, BW321, NGB 22116).

References:

1. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
2. Lundqvist, U. (Unpublished).
3. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:130.

BGS 92, Erectoides-u, *ert-u*

Stock number: BGS 92  
Locus name: Erectoides-u  
Locus symbol: *ert-u*

Previous nomenclature and gene symbolization:

Erectoides-56 = *ert-56* (3).

Brachytic 5 = *br5* (6).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2H (2); based on linkage drag with the *Gth1* (toothed lemma 1) locus (2).

Description:

Spikes are slightly denser than those of the parent with a rachis internode length estimate of 2.7 mm, and culms are about 3/4 normal length (4). Plants have a brachytic-like pattern of growth (1, 6). Spike density is decreased by GA<sub>3</sub> treatment of plants as the flag leaf emerges (5). Awns are about 3/4 normal length, and the basal rachis internode is slightly elongated.

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

*ert-u.56* (NGB 112655, GSHO 496) in Bonus (PI 189763) (3).

Mutant used for description and seed stocks:

*ert-u.56* in Bonus (NGB 112655, GSHO 496); *ert-u.56* in Bowman (PI 483237)\*8 (GSHO 1904, BW325, NGB 22120).

References:

1. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
3. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
4. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.
5. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.
6. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and erectoides mutants. *Barley Genet. Newsl.* 6:79-81.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:131.

BGS 93, Erectoides-zd, *ert-zd*

Stock number: BGS 93  
Locus name: Erectoides-zd  
Locus symbol: *ert-zd*

Previous nomenclature and gene symbolization:

Erectoides-159 = *ert-159* (5).  
Brachytic 7 = *br7* (6).

Inheritance:

Monofactorial recessive (5).  
Located in chromosome 7HL (1); *ert-zd.159* is associated with SNP markers 1\_0547 and 3\_0166 (about position 232 cM) in 7H bin 14 of the Bowman backcross-derived line BW333 (1). Previously located in chromosome 2H, based on linkage drag with the *Gth1* (toothed lemma 1) locus (4).

Description:

Plants have a brachytic-like pattern of growth and are about 3/4 normal height (3, 6). The basal rachis internode was slightly elongated. Plants of BW333, the Bowman backcross-derived line for mutant *ert-zd.159*, were 10 to 20% shorter than Bowman and the awns were about 3 cm shorter. Rachis internode lengths were slightly shorter and kernels were slightly wider for BW333 compared to those of Bowman. Kernel weights varied from slightly more to 15% less. Grain yields for BW333 varied from 1/3 to 1/2 those for Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (5).

Mutational events:

*ert-zd.159* (NGB 112758, GSHO 504) in Bonus (PI 189763) (5).

Mutant used for description and seed stocks:

*ert-zd.159* in Bonus (GSHO 504, NGB 112758); *ert-zd.159* in Bowman (PI 483237)\*7 (GSHO 1901, BW333, NGB 22128).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
5. Lundqvist, U. (Unpublished).
6. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and erectoides mutants. *Barley Genet. Newsl.* 6:79-81.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:132.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:91.

BGS 94, Albino seedling 4, *abo4*

Stock number: BGS 94  
Locus name: Albino seedling 4  
Locus symbol: *abo4*

Previous nomenclature and gene symbolization:

Albino 3 = *a3* (2).

Albino seedling 4 = *a4* (3).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 2H (1, 2); 5.0 to 10.2 cM from the *fch1* (chlorina seedling 1) locus (1, 2); about 12.5 cM from the *abo5* (albino seedling 5) locus (1).

Description:

Seedlings lack normal pigmentation; they are white and die at a two or three leaf stage (1, 2). The *abo4.d* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in an unknown cultivar (2).

Mutational events:

*abo4.d* (GSHO 167) in an unknown cultivar (1, 3).

Mutant used for description and seed stocks:

*abo4.d* (GSHO 167) in an unknown cultivar.

References:

1. Hallqvist, C. 1926. Koppelungen und synthetische Lethalität bei den Chlorophyllfaktoren der Gerste. Hereditas 8:229-254.
2. Nilsson-Ehle, H. 1922. Über freie Kombination und Koppelung verschiedener Chlorophyllerbinheiten bei Gerste. Hereditas 3:191-199.
3. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.

Prepared:

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:133.



BGS 95, Albino seedling 13, *abo13*

Stock number: BGS 95  
Locus name: Albino seedling 13  
Locus symbol: *abo13*

Previous nomenclature and gene symbolization:

Albino seedling e = *alb,,e* (1).

Albino seedling p = *alb,,p* (2).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 2HL (2); about 1.2 cM from the *msg2* (male sterile genetic 2) locus (2).

Description:

Seedlings have a white color and die at the two to three leaf stage (1). The *abo13.p* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Titan (Clho 7055) (1).

Mutational events:

*abo13.p* (GSHO 585) in Titan (1, 2); 12 additional mutants isolated in the progeny of diethyl sulfate treated *msg2* plants (generated from a cross to a balanced tertiary trisomic stock) crossed to Arivat (Clho 7543) (3, 4).

Mutant used for description and seed stocks:

*abo13.p* (GSHO 585) in Titan.

References:

1. Rahman, M.M. 1973. Balanced male sterile-lethals systems for hybrid barley production. Ph.D. Thesis. Montana State Univ., Bozeman.
2. Rahman, M.M., and R.F. Eslick. 1976. Linkage of spontaneous mutant seedling lethal genes with genetic male sterile genes. Barley Genet. Newsl. 6:53-58.
3. Ramage, R.T., and J.M. Jones. 1975. Induction of mutations for seedling lethality on chromosome 2. Barley Genet. Newsl. 5:44-45.
4. Ramage, R.T., and M.P. Scoles. 1979. Allele tests of seedling lethal mutants on chromosome 2. Barley Genet. Newsl. 9:78-79.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:134.

BGS 96, Reaction to *Puccinia hordei* 15, *Rph15*

Stock number: BGS 96  
Locus name: Reaction to *Puccinia hordei* 15 (barley leaf rust)  
Locus symbol: *Rph15*

Previous nomenclature and gene symbolization:

*Rph16* = Reaction to *Puccinia hordei* 16 (6, 9).

Inheritance:

Monofactorial dominant (1, 2).

Located in chromosome 2HS (1, 6); over 32.3 cM proximal from the *vrs1* (six-rowed spike 1) locus (1); in bin 2H-6 near molecular markers MWG874 (6) and MWG2133 (9); cosegregation with AFLP marker P13M40 (9); about 25.2cM distal from the centromere (9); about 14 cM proximal from the *Eam1* (Early maturity 1) locus (3).

Description:

The seedling reaction to most isolates of *Puccinia hordei* is a relatively large necrotic fleck, hypersensitive reaction (1). The seedling infection type of heterozygotes is indistinguishable from that of homozygous resistant seedlings. Alleles at this locus were found in six of the first seven *Rph* genes from *Hordeum vulgare* subsp. *spontaneum* evaluated in Bowman backcross-derived lines (1, 2). The *Rph15* locus is likely allelic to *Rph16* based on the failure to recover susceptible recombinants (9). Only one of the 350 leaf rust isolates (90-3 from Israel) was found to be virulent on *Rph15* lines (4, 9).

Resistance to isolate 90-3 was observed in progeny from a cross between a line with *Rph15* to another source of leaf rust resistance (8). *Rph15* represents one of the most effective leaf rust resistance genes reported in *Hordeum vulgare* (9).

Origin of mutant:

Natural occurrence in accession PI 355447 of *Hordeum vulgare* subsp. *spontaneum*, but isolated in a selection that contained one *Rph* gene from the original accession crossed to Bowman (PI 483237) (1, 7).

Mutational events:

*Rph15.ad* in PI 355447 (GSHO 1586) (1, 2, 5), PI 354937, PI 391024, PI 391069, PI 391089, and PI 466245 (1, 2); *Rph15.ae* from HS084 (6, 9); PI 466245 has at least two genes for leaf rust resistance (7).

Mutant used for description and seed stocks:

*Rph15.ad* PI 355447 (GSHO 1586); *Rph15.ad* from PI 355447 in Bowman\*8 (GSHO 2330, PI 643164, BW719, NGB 33425). (The *Rph15.ad* gene from other *Hordeum vulgare* subsp. *Spontaneum* accessions may be present in about 40 other BW lines).

References:

1. Chicaiza, O. 1996. Genetic control of leaf rust in barley. Ph.D. dissertation, North Dakota State Univ., Fargo.
2. Chicaiza, O., J.D. Franckowiak, and B.J. Steffenson. 1996. New sources of resistance to leaf rust in barley. pp. 706-708. In A.E. Slinkard, G.J. Scoles, and B.G. Rossnagel (eds.). Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp., Saskatoon. Univ. of Saskatchewan, Saskatoon.
3. Falk, A.B. (Personal communications).
4. Fetch, T.G. Jr., B.J. Steffenson, and Y. Jin. 1998. Worldwide virulence of *Puccinia hordei* on barley. Phytopathology 88:S28.
5. Franckowiak, J.D., Y. Jin, and B.J. Steffenson. 1997. Recommended allele symbols for leaf rust resistance genes in barley. Barley Genet. Newsl. 27:36-44.
6. Ivandic, V., U. Walther, and A. Graner. 1998. Molecular mapping of a new gene in wild barley conferring complete resistance to leaf rust (*Puccinia hordei* Otth). Theor.

Appl. Genet. 97:1235-1239.

7. Jin, Y., and B.J. Steffenson. 1994. Inheritance of resistance to *Puccinia hordei* in cultivated and wild barley. J. Hered. 85:451-454.

8. Sun, Y., J.D. Franckowiak, and S.M. Neate. 2005. Reactions of barley lines to leaf rust, caused by *Puccinia hordei*. Proceedings of the 18th [North American Barley Researchers Workshop](#), July 17-20, 2005, Red Deer, Alberta, Canada

[http://www1.agric.gov.ab.ca/\\$department/deptdocs.nsf/all/fcd10135#Reactions](http://www1.agric.gov.ab.ca/$department/deptdocs.nsf/all/fcd10135#Reactions)

9. Weerasena, J.S., B.J. Steffenson, and A.B. Falk. 2004. Conversion of an amplified fragment length polymorphism marker into a co-dominant marker in the mapping of the *Rph15* gene conferring resistance to barley leaf rust, *Puccinia hordei* Otth. Theor. Appl. Genet. 108:712-719.

Prepared:

J.D. Franckowiak and O. Chicaiza. 1998. Barley Genet. Newsl. 28:29.

Revised:

J.D. Franckowiak. 2005. Barley Genet. Newsl. 35:186.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:214-215.

BGS 97, Accordion rachis 1, *acr1*

Stock number: BGS 97  
Locus name: Accordion rachis 1  
Locus symbol: *acr1*

Previous nomenclature and gene symbolization:

Lax rachis internode = *ril* (2).

Accordion rachis = *acr* (5, 6).

Inheritance:

Monofactorial recessive (2, 5, 6), part of a multiple genic series involving *acr1*, *acr2* and *acr3* required for expression (3).

Located in chromosome 2HL (3); near the *vrs1* (six-rowed spike 1) locus because no recombination with the *Vrs1.t* (deficiens) allele was observed (3); associated with SNP markers 1\_0525 to 2\_0667 (positions 65.03 to 117.73 cM) in 2H of the Bowman backcross-derived lines BW009 and BW439 (1), likely in 2H bins 06 to 08.

Description:

Rachis internodes are greatly elongated and often bent or pleaded as the spike emerges from the boot or sheath of the flag leaf (5). The line ACBV89B229, developed by R.I. Wolfe to maximize rachis internode length, exhibits extreme elongation of rachis internodes, rachis internode length values up to 7.7 mm, and occasionally trapping of the spike tip in the boot (3, 7). Elongation of the rachis internodes is associated with slightly elongated outer glumes and the deficiens (*Vrs1.t*) spike phenotype. Two modifiers, *acr2* (see BGS 189) and *acr3* (see BGS 241), caused variable expression of the accordion trait in different genetic backgrounds. In crosses to Bowman, segregation for *acr1* fit a three gene model based on DNA segments retained in the Bowman backcross-derived lines BW009 and BW439 (1, 3). Although the *acr1* gene is apparently associated with the deficiens spike type, the large centromeric segment of 2H retained does not overlap the six-rowed spike 1 (*vrs1*) locus (1). A pericentric inversion can not be eliminated as a possibility. Plants in the BW009 and BW439 lines were about 3/4 of normal height and peduncles were about 1/2 of normal length. The number of fertile rachis nodes was reduced by about 3 and heading was delayed by up to 4 days. Kernels appeared thinner and weighted about 10% less. Test weights were low and grain yield was about 3/4 of normal (3).

Origin of mutant:

A naturally occurring deviant (4) incorporated into several genetic stocks, *acr1.a* in Beaverlodge stock ACBV89B229 was used to study this locus (3, 7).

Mutational events:

*acr1.a* in ACBV89B229 (GSHO 1617) and ACBV89232 (GSHO 1573) (7).

Mutant used for description and seed stocks:

*acr1.a* in ACBV89B229 (GSHO 1617); *acr1.a* in Bowman (PI 483237)\*4 (GSHO 1899); *acr1.a* in Bowman\*7 (BW009, NGB 20417 and BW439, NGB 20671).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Enns, H. 1961. Inheritance and linkage studies in barley using chromosomal interchanges and marker stocks. Ph.D. Thesis. Univ. Saskatchewan. pp. 70.
3. Franckowiak, J.D. (Unpublished).

4. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
5. Haus, T.E. 1957. Inheritance of rachis internode length and an abnormal rachis type in barley. *Dissertation Abstr.* 49:179-180.
6. Nilan, R.A. 1964. The cytology and genetics of barley, 1951-1962. *Monogr. Suppl.* 3, *Res. Stud.* Vol. 32, No. 1. Washington State Univ. Press, Pullman.
7. Wolfe, R.I. 1990. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:85.

Revised:

J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:56-57.

BGS 98, Early maturity 6, *Eam6*

Stock number: BGS 98  
Locus name: Early maturity 6  
Locus symbol: *Eam6*

Previous nomenclature and gene symbolization:

Early heading = *Ea* (9).  
Early maturity 6 = *Ea6* (7).

Inheritance:

Monofactorial dominant (9).  
Located in chromosome 2HS (9); about 13.5 cM proximal from the *vrs1* (six-rowed spike 1) locus (9); near the *gsh5* (glossy sheath 5) locus based on linkage drag (1, 2); near molecular marker ABC167b in 2H bin 08 (5, 8).

Description:

Alleles at the *Eam6* locus alter the timing of floral initiation when barley is grown under long-day conditions. In temperate climates, the *Eam6.h* gene induces spring barley to head two to five days earlier than plants with the recessive allele (1, 5). A much stronger response to long photoperiods is associated with the *Eam1* gene. Tohno-oka et al. (8) reported that *Eam6* gene from Morex (CIho 15773) is effective when the photoperiod is 13 hours or longer and that the *Eam1* gene from Steptoe (CIho 15229) induces early heading when the photoperiod is 14 hours or longer. In North Dakota, plants with both the *Eam1* and *Eam6* genes head one to two days earlier than those with only the *Eam1* gene (1). The factors, *Eam1* and *Eam6*, for early heading were studied possibly by Yasuda (10) and named "A" and "B", respectively. A QTL for long-day photoperiod response in North American two-rowed and six-rowed barleys in the *Eam6* region of 2H was reported by Moralejo et al. (6) and Horsley et al. (3), respectively. *Eam6* may interact with other maturity genes because a QTL for early heading was detected in 2HS under both short- and long-day environments in the Harrington/Morex mapping population (4).

Origin of mutant:

Natural occurrence in many spring, six-rowed barley, represented by the cultivar Morex (CIho 15773) (8).

Mutational events:

*Eam6.h* in an unknown cultivar (8), possibly Trebi (CIho 936) (1); *Eam6.h* in Morex (CIho 15773) (4, 5, 8).

Mutant used for description and seed stocks:

*Eam6.h* in Morex (CIho 15773, GSHO 2492); *Eam6.h* from Nordic (CIho 15216) is present in Bowman (PI 483237) (1).

References:

1. Franckowiak, J.D., and G. Yu (Unpublished).
2. Franckowiak, J.D., and U. Lundqvist. 1997. BGS 355, glossy sheath 5, *gsh5*. Barley Genet. Newsl. 26:300-301.
3. Horsley, R.D., D. Schmierer, C. Maier, D. Kudrna, C.A. Urrea, B.J. Steffenson, P.B. Schwarz, J.D. Franckowiak, M.J. Green, B. Zhang, and A. Kleinhofs. 2006. Identification of QTLs associated with Fusarium head blight resistance in barley accession CIho 4196. Crop Sci. 46:145-156.
4. Krasheninnik, N. 2005. Genetic association of Fusarium head blight resistance and morphological traits in barley. Ph.D. Thesis. North Dakota state Univ., Fargo, ND.
5. Marquez-Cedillo, L.A., P.M. Hayes, A. Kleinhofs, W.G. Legge, B.G. Rossnagel, K. Sato, S.E. Ullrich, and D. M. Wesenberg. 2001. QTL analysis of agronomic traits in

barley based on the doubled haploid progeny of two elite North American varieties representing different germplasm groups. Theor. Appl. Genet. 103:625-637.

6. Moralejo, M., J.S. Swanston, P. Muñoz, D. Prada, M. Elía, J.R. Russell, L. Ramsay, L. Cistué, P. Codesal, A.M. Casa, I. Romagosa, W. Powell, and J.L. Molina-Cano. 2004.

Use of new EST markers to elucidate the genetic differences in grain protein content between European and North American two-rowed malting barleys. Theor. Appl. Genet. 110:116-125.

7. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III, 1954-1963. Crop Sci. 5:33-43.

8. Tohno-oka, T., M. Ishit, R. Kanatani, H. Takahashi, and K. Takeda. 2000. Genetic analysis of photoperiodic response of barley in different daylength conditions. p. 239-241. In S. Logue (ed.) Barley Genetics VIII. Volume III. Proc. Eighth Int. Barley Genet. Symp., Adelaide. Dept. Plant Science, Waite Campus, Adelaide University, Glen Osmond, South Australia.

9. Woodward, R.W. 1957. Linkages in barley. Agron. J. 49:28-32.

10. Yasuda, S. 1958. (Genetic analysis of the response to short photoperiod in a barley cross by means of the partitioning method.) Nogaku Kenkyu 46:54-62 [In Japanese].

Prepared:

J.D. Franckowiak and T. Konishi. 2002. Barley Genet. Newsl. 32:86-87.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:216-217.

BGS 99, Lesser internode number 1, *lin1*

Stock number: BGS 99  
Locus name: Lesser internode number 1  
Locus symbol: *lin1*

Previous nomenclature and gene symbolization:

Rachis internode number = *s*, *rin* (3, 6).  
Low number of rachis internodes = *rin* (4).  
Rachis internode length QTL on 2H = *qSIL.ak-2H* (5).

Inheritance:

Monofactorial recessive (6, 7).  
Located in chromosome 2HS (7); about 15.1 cM distal from the *eog1* (elongated outer glume 1) locus and about 17.1 cM proximal from the *vrs1* (six-rowed spike 1) locus (6); about 6 cM proximal from STS marker ABG602 and the *Eam1* (early maturity 1) locus (5), likely in 2H bin 07.

Description:

The mean number of rachis internodes per spike is reduced by 20 to 40% (6, 7). The average internode number was 15.3 in Triple Bearded Mariout and 22.9 in Spartan (6). Presence of the *Eam1* (early maturity 1) gene closely linked to *lin1.a* gene in Triple Bearded Mariout (BGS 57) made study of *lin1* locus difficult in some environments; therefore, a new BGS number was recommended (2). In some six-rowed cultivars such as Morex, the reduction in rachis internodes associated with the *lin1* gene is less obvious (1). A significant reduction triplet number, 1.5 to 2.3 fertile rachis nodes, was associated with the Azumamugi allele in 2HS and mapped near the *Eam1* (early maturity 1) locus (5). Since mapping population was grown under short-day conditions, the effects of the *Eam1* gene on maturity and plant development were not expressed (5). The effects of alleles at the *lin1* locus on fertile rachis nodes are more obvious when barley is grown in heat stressed environments. Fewer fertile rachis nodes per spike may lead to plumper kernels. The *lin1.a* gene is likely present in Bowman and may be associated with tolerance to heat stress (1).

Origin of mutant:

Natural occurrence in many six-rowed barley cultivars of North African and Asian origin (1). Tavcar's mutant stock is no longer available.

Mutational events:

*lin1.a* in Triple Bearded Mariout (CIho 2523, GSHO 29) (6).

Mutant used for description and seed stocks:

*lin1.a* in Morex (CIho 15773, GSHO 2492); *lin1.a* from Nordic (CIho 15216) is present in Bowman (PI 483237).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 2002. BGS 99, Lesser internode number 1, *lin1*. Barley Genet. Newsl. 32:88.
3. Freisleben, R., and I. Metzger. 1942. Genetische Studien zur Gerstenzüchtung. I. Vererbung und Koppelung der Mehltreueresistenz und der Spindelgliedzahl. Z. f. Pflanzenzücht. 24:507-522.
4. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.
5. Sameri, M., K. Takeda, and T. Komatsuda. 2006. Quantitative trait loci controlling agronomic traits in recombinant inbred lines from a cross of oriental- and occidental-type barley cultivars. Breed. Sci. 56:243-252.



6. Swenson, S.P., and D.G. Wells. 1944. The linkage relation of four genes in chromosome 1 of barley. J. Am. Soc. Agron. 36:429-435.

7. Tavcar, A. 1938. Vererbungsart der Spindelstufenzahl bei Bastardierungen einiger *distichum* x *vulgare* Wintergersten. Z. Indukt. Abstammungs. Vererbungs. 75:106-123.

Prepared:

T. Tsuchiya and T.E. Haus. 1971 Barley Genet. Newsl. 1:117 as BGS 57, Reduced internode number, *rin*.

Revised:

T. Tsuchiya and T.E. Haus. 1984. Barley Genet. Newsl. 14:91 as BGS 57, Lesser internode number, *lin*.

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:88: BGS number changes from BGS 57 to BGS 99.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:92-93.

BGS 100, Slender dwarf 4, *sld4*

Stock number: BGS 100  
Locus name: Slender dwarf 4  
Locus symbol: *sld4*

Previous nomenclature and gene symbolization:

Slender dwarf d = *sld.d* (2).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 2HS (5); located in chromosome 7HS (4); near AFLP marker E 4134-2 in subgroup 6 of the Proctor/Nudinka map (4).

Description:

Plants with the *sld4.d* gene have reduced vigor and are light green in color during early stages of growth (6). The *sld4.d* mutant is apparently very environmentally sensitive in the Bowman derived line. Plants can vary from less than 1/2 to 3/4 of normal height and heading can be delayed over 10 days in certain environments. The number of fertile spikelets per spike varies from 2/3 normal to near normal. Depending on the delay in heading, kernels vary from very thin to near normal. Grain yield of the Bowman backcross-derived line can vary from very low to nearly normal (1).

Origin of mutant:

A neutron induced mutant in Two-row Glacier (Clho 16615) (5). (Glacier is available as Clho 6976.)

Mutational events:

*sld4.d* (80-T-5899-2-13, DWS1368, GSHO 2479) in Two-row Glacier (Clho 16615) (2, 3, 5).

Mutant used for description and seed stocks:

*sld4.d* (GSHO 2479) in Two-row Glacier; *sld4.d* in Bowman (PI 483237)\*7 (GSHO 1880, BW864, NGB 22301).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1999. Coordinator's report: Semidwarf genes. Barley Genet. Newsl. 29:74-79.
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
5. Ramage, R.T., and P. Curtis. 1981. A light green, dwarf mutant located on chromosome 2. Barley Genet. Newsl. 11:37-38.
6. Ramage, R.T., and R.A. Ronstadt-Smith. 1983. Location of a light green dwarf mutant on chromosome 2. Barley Genet. Newsl. 13:62-64.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:89.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:218.